

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2004, 23:42:47 ; Search time 2250 Seconds  
(without alignments)  
10267.483 Million cell updates/sec

Title: US-10-623-891-2  
Perfect score: 533  
Sequence: 1 tctggggaggagagctccg999.....cgtgagatcttcggtacacaa 533

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl :  
1: gb\_ba :  
2: gb\_hlg :  
3: gb\_in :  
4: gb\_cm :  
5: gb\_ov :  
6: gb\_pac :  
7: gb\_ph :  
8: gb\_pl :  
9: gb\_pr :  
10: gb\_ro :  
11: gb\_sts :  
12: gb\_sy :  
13: gb\_un :  
14: gb\_vl :  
15: gb\_ba :  
16: gb\_fun :  
17: gb\_hum :  
18: gb\_in :  
19: gb\_mu :  
20: gb\_ov :  
21: gb\_or :  
22: gb\_ov :  
23: gb\_pac :  
24: gb\_ph :  
25: gb\_pl :  
26: gb\_ro :  
27: gb\_sts :  
28: gb\_un :  
29: gb\_vl :  
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34: gb\_hlg :  
35: gb\_hlg :  
36: gb\_hlg :  
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39: gb\_hlg :  
40: gb\_hlg :  
41: gb\_hlg :

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	100.0	585	14	S82226
2	507.8	95.3	1005	14	ACRLTR1
3	506	94.9	4232	14	AF006065
4	506	94.9	8221	14	AF246698
5	503	94.4	887	14	ACRLTR2
6	490.8	92.1	745	14	AY255632
7	439.4	82.4	940	6	BD006232
8	438.4	82.3	545	14	S70398
9	429	80.5	583	14	S79845
10	313.8	58.9	859	14	REXXX2
11	313.8	58.9	891	14	REXXX1
12	206.4	38.7	1032	14	AF006066
13	193	36.2	465	14	AY255633
14	193	36.2	2640	14	AF006064
15	193	36.2	288539	14	AF198100
16	155	29.1	578	6	A83549
17	155	29.1	578	6	BD006233
18	130.4	24.5	1530	14	RESNVX
19	119.6	22.4	160	5	CHKSNTA2
20	119.6	22.4	160	5	CHKSNTA2
21	119.6	22.4	160	5	CHKSNTA2
22	119.6	22.4	160	5	CHKSNTA2
23	119.6	22.4	160	5	CHKSNTA2
24	119.6	22.4	160	5	CHKSNTA2
25	119.6	22.4	160	5	CHKSNTA2
26	106.2	19.9	180	14	SNVTR
27	80.8	15.2	163	14	SNVTRMB
28	64.8	12.2	100	14	SNVTR12
29	58.4	11.0	209	14	SNVTRMA
30	44.8	8.4	69	5	CHKSNTA1
31	42.6	8.0	69	5	CHKSNTA1
32	42.6	8.0	69	5	CHKSNTA1
33	42.6	8.0	69	5	CHKSNTA1
34	42.2	7.9	69	5	CHKSNTA1
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36	40.4	7.6	100	14	SNVTR11
37	39.6	7.4	155853	5	AL935041
38	39.6	7.4	167563	5	AL928838
39	39.6	7.4	182325	5	BX004869
40	39.6	7.4	189694	2	BX005365
41	39.6	7.4	207161	2	BX530067
42	39.6	7.4	211383	2	BX119319
43	39.6	7.4	219981	2	BX544872
44	39.6	7.4	224806	2	BX004858
45	39.2	7.4	237323	10	AL772376

## ALIGNMENTS

RESULT 1  
LOCUS S82226 585 bp DNA linear VRL 12-FEB-1997  
DEFINITION (RS region, intervening sequence) [Marek's disease virus MDV, RML,  
Genomic DNA, 585 nt].  
ACCESSION S82226  
VERSION S82226.1 GI:1839499  
KEYWORDS Gallid herpesvirus 2  
SOURCE Gallid herpesvirus 2  
ORGANISM Gallid herpesvirus 2  
vireuses; debDNA vireuses, no RNA stage; Herpesviridae;  
Alphaherpesvirinae; Marek's disease-like vireuses.  
REFERENCE 1 (bases 1 to 585)  
AUTHORS 'Jones,D.,Brunovskis,P.,Witter,R. and Kung,H-J',  
TITLE 'Retroviral-inertional-activation-in-a-herpesvirus-transcriptional

Pred. No. is the number of results predicted by chance to have a

activation of US genes by an integrated long terminal repeat in a Marek's disease virus clone  
J. Virol. 70 (4), 2460-2467 (1996)

JOURNAL  
MEDLINE  
PUBMED  
8642673

GenBank staff at the National Library of Medicine created this entry [NCBI gi18131] from the original journal article.

Authors indicate intervening sequence from nt 23 to nt 555 inclusive derived from co-infecting reticuloendotheliosis virus strain CSV.

## FEATURES

Source

## ORIGIN

Query Match 100.0%; Score 533; DB 14; Length 585;  
Best Local Similarity 100.0%; Pred. No. 4.7e-153;  
Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TGTGGAGGAGAGCTCCGGGGAATGAGGAGAGAGCTCCGGGGGAATAGCGCTGCG 60  
23 TGTGGAGGAGAGCTCCGGGGAATGAGGAGAGAGCTCCGGGGGAATAGCGCTGCG 82  
61 CTAACTGCGCATTTAGCTTCTGTAATCAATGCTTGTGCTTGGCGGCGCATTTGTA 120  
83 CTAACTGCGCATTTAGCTTCTGTAATCAATGCTTGTGCTTGGCGGCGCATTTGTA 142  
121 TATATTTGCTGATTCATTTCTCGGANTCGGANTCAAGAGAGAGCTCATTAACCTAAA 180  
143 TATATTTGCTGATTCATTTCTCGGANTCGGANTCAAGAGAGAGCTCATTAACCTAAA 202  
161 AGGAATGTTGTTGAGGAGAGAGATCAAGACCATTTGACCATTCATCAAGAGAGAG 240  
203 AGGAATGTTGTTGAGGAGAGAGATCAAGACCATTTGACCATTCATCAAGAGAGAG 262  
241 CGAGATCGACATTCATTCAGGAGAGAGATGTTGTAAGAGGAGAGATGTTGTTGTA 300  
263 CGAGATCGACATTCATTCAGGAGAGAGATGTTGTAAGAGGAGAGATGTTGTTGTA 322  
301 GGGAAATGTCATCAACATCTGTAAAGCGGCTTATTAAGCGAGTGCATCTTGTGCG 360  
323 GGGAAATGTCATCAACATCTGTAAAGCGGCTTATTAAGCGAGTGCATCTTGTGCG 382  
361 GGGCGCGGCTTATTAAGCGGAGATGTTGTAAGCGGCGGCGGAGTGCATCTTGTGCG 420  
383 GGGCGCGGCTTATTAAGCGGAGATGTTGTAAGCGGCGGCGGAGTGCATCTTGTGCG 442  
421 TTTTCTTCTATATCTCAAGATTGGAGAGAGAGATTTGTTGTTGTTGTTGTTGTTG 480  
443 TTTTCTTCTATATCTCAAGATTGGAGAGAGAGATTTGTTGTTGTTGTTGTTGTTG 502  
481 CCTACTGGGAGGAGATCCGAGCTGAATCCGTAATTTTGGTACAA 533  
503 CCTACTGGGAGGAGATCCGAGCTGAATCCGTAATTTTGGTACAA 555

RESULT 2  
ACRLTRI 1005 bp ss-RNA linear VRL 27-APR-1993  
LOCUS Reticuloendotheliosis virus 713 proviral clone RNA.  
DEFINITION M2223.1 GI:209708  
VERSION M2223.1 GI:209708  
KEYWORDS long terminal repeat (LTR).  
SOURCE Reticuloendotheliosis virus  
ORGANISM Reticuloendotheliosis virus  
VIRUSES: Retrod viruses; Retroviridae; Gammaretrovirus.  
1 (bases 99 to 195)  
Ridgway,A., Swift,R.A., Kung,H.J., and Fujita,D.J.  
In vitro transcription analysis of the viral promoter involved in c-myc activation in chicken B lymphomas: detection and mapping of

two RNA initiation sites within the reticuloendotheliosis virus long terminal repeat  
J. Virol. 54 (1), 161-170 (1985)

JOURNAL  
MEDLINE  
PUBMED  
2983111

2 (bases 1 to 1005)  
Swift,R.A., Boerkoel,C., Ridgway,A., Fujita,D.J., Dodgson,J.B. and Kung,H.J.  
B-lymphoma induction by reticuloendotheliosis virus: characterization of a mutated chicken syncytial virus provirus involved in c-myc activation

J. Virol. 61 (7), 2084-2090 (1987)

## FEATURES

Source

Original source text: Reticuloendotheliosis virus (from chicken line 151-5 B lymphomas), cDNA to mRNA, clone 713.

## ORIGIN

Query Match 95.3%; Score 507.8; DB 14; Length 1005;  
Best Local Similarity 99.6%; Pred. No. 2.9e-145;  
Matches 509; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

19 bp upstream of SacI site.  
LTR  
23 ATGTGGAGGAGAGCTCCGGGGAATAGGAGAGAGCTCCGCTGCTCAATGCGCATTTAGCT 82  
5 ATGTGGAGGAGAGCTCCGGGGAATAGGAGAGAGCTCCGCTGCTCAATGCGCATTTAGCT 64  
83 TATCATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 142  
65 TATCATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 124  
143 TCGGAATGCGGATCAAGAGAGAGCTCAATTAACCTAAAGAAATGTTGTTGAGGCAA 202  
125 TCGGAATGCGGATCAAGAGAGAGCTCAATTAACCTAAAGAAATGTTGTTGAGGCAA 184  
203 GCATCAAGCACTTGACCATTCATCAAGAGAGAGAGATGCAATGCAATGCAATGCA 262  
185 GCATCAAGCACTTGACCATTCATCAAGAGAGAGAGATGCAATGCAATGCAATGCA 244  
263 GCATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 322  
245 GCATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 304  
323 TGTAAAGCGGCTATTAAGCGAGAGTGCATCTTGTGCTGAGGAGTGCATCAATTTG 382  
305 TGTAAAGCGGCTATTAAGCGAGAGTGCATCTTGTGCTGAGGAGTGCATCAATTTG 364  
383 TGTAAAGCGGCGGCGGAGATTCGAAATCTGTAATTAAGAGTTTCTTCTATATCTCAGAT 442  
365 TGTAAAGCGGCGGCGGAGATTCGAAATCTGTAATTAAGAGTTTCTTCTATATCTCAGAT 424  
443 TGTAAAGCGGAGAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 502  
425 TGTAAAGCGGAGAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 484  
503 CGAGCTGAATCCGTAATTTTGGTACAA 533  
485 CGAGCTGAATCCGTAATTTTGGTACAA 515

RESULT 3  
AF006065 4292 bp DNA linear VRL 16-SEP-1997  
LOCUS Fowlpox virus S gag gene, complete cds, and protease/polymerase  
DEFINITION (pro/pol) gene, partial cds.  
ACCESSION AF006065  
VERSION AF006065.1 GI:2393892

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
Fowlpox virus
Fowlpox virus
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Avipoxvirus.
1 (bases 1 to 4292)
Hettig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.
Field and vaccine strains of fowlpox virus carry integrated
sequences from the avian retrovirus, reticuloendotheliosis virus
Virology 235 (2), 367-376 (1997)
97428585
9281517
2 (bases 1 to 4292)
Hettig,C.H., Coupar,B.E.H., Gould,A.R. and Boyle,D.B.
Direct Submission Division of Animal Health, CSIRO, 5
Submitted (30-MAY-1997) Geelong, Victoria 3213, Australia
Portarlington Road,
Location/Qualifiers
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Ltd, Castle Hill, New South Wales, Australia.
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Query Match	Similarity	94.9%; Score 506; DB 14; Length 4297;
Best Local	Similarity	100.0%; Prod. No. 1,1e-144;
Matches	506; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	28	GAAGAGAGCTCCGGGGGAAATAGCGCTGCTCGCTAACTGGCATATTAAGTTCTGTATTC 87
DB	908	GAAGAGAGCTCCGGGGGAAATAGCGCTGCTCGCTAACTGGCATATTAAGTTCTGTATTC 967
QY	88	ATGCTTGTTCCTTAAAGCCGCAATTTGAATCTGATATATTTGGCGATATATCTTTCTGGG 147
DB	968	ATGCTTGTTCCTTAAAGCCGCAATTTGAATCTGATATATTTGGCGATATATCTTTCTGGG 1027
QY	148	ATTCGCATCAAGAGAGAGCTCATTAACCATTAAGAAATGTTGTTGAAGCAAGCATC 207
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QY	208	AGACCACCTTGCACCATCCATCAAGAAACAAACAGAGTCGAACTATCATCTAGCCAA 267
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QY	268	TGTTTGTAAAGGAGAGATGCTATCTCTCCATAGAGGAAATGTATGCAACATCTCTGTA 327
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QY	328	GCGGCTATATAGCAGAGTGCATCTCTGCTCGGGGGTCGCGCTCAACATCTGTTGTA 387
DB	1208	GCGGCTATATAGCAGAGTGCATCTCTGCTCGGGGGTCGCGCTCAACATCTGTTGTA 1267
QY	388	CGTCGCGCCAGATTCGATCTGTATATTAAGATTTTTCCTCTATCTTCAGATTGGCA 447
DB	1268	CGTCGCGCCAGATTCGATCTGTATATTAAGATTTTTCCTCTATCTTCAGATTGGCA 1327
QY	448	GTGAGAGAGATTTTTCCTGTTGTTGGCTGCGCTCACTGGGTGGGGTAGGAGATCCGAG 507
DB	1328	GTGAGAGAGATTTTTCCTGTTGTTGGCTGCGCTCACTGGGTGGGGTAGGAGATCCGAG 1387
QY	508	TGAATCCCTACTATTTGGGTACA 533
DB	1388	TGAATCCCTACTATTTGGGTACA 1413
RESULT 4		
AF246698		
LOCUS	AF246698	8221 bp DNA linear VRL 12-MAR-2003
DEFINITION	Fowlpox virus hypothetical protein gene, partial cds, integrated	
	Reichleidoendoheliosis provirus, complete sequence; and protein	
	kinase-like protein gene, partial cds.	
VERSION	AF246698	
KEYWORDS	AF246698.2 GI:28927668	
SOURCE		
ORGANISM	Fowlpox virus	
	Fowlpox virus	
	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
	Avipoxvirus.	
REFERENCE	1 (bases 1 to 8221)	
AUTHORS	Singh, P., Kim, T.-J. and Tripathy, D.N.	
TITLE	Re-emerging fowlpox: evaluation of isolates from vaccinated flocks	
JOURNAL	Avian Pathol. 29, 449-455 (2000)	
AUTHORS	2 (bases 1 to 8221)	
TITLE	Singh, P., Schitzlein, W.M. and Tripathy, D.N.	
	Reichleidoendoheliosis Virus Sequences Within the Genomes of Field	
	Strains of Fowlpox Virus Display Variability	
	J. Virol. (2003) In press	
JOURNAL	3 (bases 1 to 8221)	
REFERENCE	Schitzlein, W.M., Srinivasan, V. and Tripathy, D.N.	
AUTHORS	Direct Submission	
TITLE	Submitted (16-MAR-2000) Veterinary Pathobiology, University of	
JOURNAL	Illinois, 2001 South Lincoln Avenue, Urbana, IL 61802, USA	
AUTHORS	4 (bases 1 to 8221)	
TITLE	Schitzlein, W.M., Singh, P., Srinivasan, V. and Tripathy, D.N.	
JOURNAL	Direct Submission	
	Submitted (12-MAR-2003) University of Illinois at Urbana-Champaign,	
	2001 South Lincoln Avenue, Urbana, IL 61802, USA	

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REMARK      Sequence update by submitter
COMMENT      On Mar 12, 2003 this sequence version replaced gi:8926141.
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  KRVAVALSKRLDPVAGMPCRLAIAAALLTREASKLTFGGDIETSSHNSLELRS
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  STRPDLTQPLQAEATLFTDGSYAIRBCKRYTGAAVTVDSVIAEELPIGTBQKA
  EILATLKALEMSKDSKSVNTYDSRYAFATLHGMATYRRGLITGSAIKNAPEILA
  LITAVMLPRVAVMCKGQKQKADPATSTGNRPADEVAEVALRPLSTQATTSADPMP
  DNETPOYSVBEALGRLNGTDQPAQMMWLPGRLLLPRAVAKRLQETHRAITGYES
  KLELVKRYHLICGIRARADITTRCAQAVNPATPEVEKANGIRGAAPGHEWV
  DTEWNTAKGKYKYLIVDTFSGWNEVAPARSTSOVYIKLIDHILPRFLPGIOG
  SINGEASVAKVTOQLCEALNWMKLCAGVAPSSQVBRMNRLLKETIAKRIETGSD
  WSLPQALRLARCTPGREGASPEFIVLGIDKPPVPRVGCCKLASITNQTLLKSQAL
  QATRSILARALADLOLPOKEAODRPTPLQPGDLVVKADHQQGLSPRMDGYTVVLST
  PPAVAVAGCTPVIHHSRLKKAAPDNOEEMWTSFTSDPLKVLTRAKP"
  5990..7750
    /note="env"
    /codon_start=1
    /product="envelope glycoprotein"
    /protein_id="AA061698.2"
    /db_xref="GI:28927670"
ORIGIN
Query Match      94.9%; Score 506; DB 14; Length 8221;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  28  GGAGGAGAGCTCCGGGGGGAATAGCGCTGCTGCTAATCTCCATATTAAGCTTGTATATC 87
  68  GGAAGGAGAGCTCCGGGGGGAATAGCGCTGCTGCTAATCTCCATATTAAGCTTGTATATC 127
  88  ATGCTTGTGCTGCTTGAAGCGGCAATGTACTGTATATATTTGGCGATATCAATTTCTGGA 147
  128  ATGCTTGTGCTGCTTGAAGCGGCAATGTACTGTATATATTTGGCGATATCAATTTCTGGA 187
  148  ATTCGCATCAAGAGAGGCTCATTAACCAATAAAGAAATGTTTGTGAAGGCAAGCATC 207
  188  ATTCGCATCAAGAGAGGCTCATTAACCAATAAAGAAATGTTTGTGAAGGCAAGCATC 247
  208  AGACCACTTGACACCATCCATCAAGAAACAAACAGAGATGCACTATCATCTAGAGCA 267
  248  AGACCACTTGACACCATCCATCAAGAAACAAACAGAGATGCACTATCATCTAGAGCA 307
  268  TGGTTGTAAAGGAGAGATGCTATCTCAATGAAGGAAAAATGTCATGCAACATCTGTAA 327
  308  TGGTTGTAAAGGAGAGATGCTATCTCAATGAAGGAAAAATGTCATGCAACATCTGTAA 367
  328  GCGGCTATATTAAGGAGAGATGCTATCTCAATGAAGGAAAAATGTCATGCAACATCTGTAA 387
  368  GCGGCTATATTAAGGAGAGATGCTATCTCAATGAAGGAAAAATGTCATGCAACATCTGTAA 427
  388  GGTGCGGCGCCAGATTCGATCTGTAATAAAGCTTTTCTTATATATCCAGATTGGCA 447
  428  GGTGCGGCGCCAGATTCGATCTGTAATAAAGCTTTTCTTATATATCCAGATTGGCA 487
  448  GTGAGAGAGATTTTGTCTGTGTGTGGTGCGCTACGAGTGAGGATGAGATCCGAGC 507
  488  GTGAGAGAGATTTTGTCTGTGTGTGGTGCGCTACGAGTGAGGATGAGATCCGAGC 547
  508  TGAATCGTAGTATTTCCGTACACA 533
  548  TGAATCGTAGTATTTCCGTACACA 573
RESULT 5
ACRLTR2      887 bp ss-RNA, linear   VRL 27-APR-1993
LOCUS        Reticuloendotheliosis virus 713 proviral clone RNA.
DEFINITION   M22224 M10660 M16722
ACCESSION   M22224.1 GI:209709
VERSION      long terminal repeat (LTR).
KEYWORDS     Reticuloendotheliosis virus
SOURCE       Reticuloendotheliosis virus
ORGANISM     Viruses; Retroviridae; Gammaretrovirus.
REFERENCE    1 (bases 510 to 602)
```

**AUTHORS** Ridgway,A.A., Swift,R.A., Kung,H.J. and Fujita,D.J.  
**TITLE** In vitro transcription analysis of the viral promoter involved in c-myc activation in chicken B lymphomas: detection and mapping of two RNA initiation sites within the reticuloendotheliosis virus long terminal repeat  
**JOURNAL** J. Virol. 54 (1), 161-170 (1985)  
**MEDLINE** 85135063  
**PUBMED** 2983111  
**REFERENCE** 2 (bases 1 to 887)  
**AUTHORS** Swift,R.A., Boerkoel,C., Ridgway,A., Fujita,D.J., Dodgson,J.B. and Kung,H.J.  
**TITLE** B-lymphoma induction by reticuloendotheliosis virus: characterization of a mutated chicken syncytial virus provirus involved in c-myc activation  
**JOURNAL** J. Virol. 61 (7), 2084-2090 (1987)  
**MEDLINE** 8726389  
**PUBMED** 3035210  
**COMMENT** Original source text: Reticuloendotheliosis virus (from chicken line 151-5 B lymphomas), cDNA to mRNA, clone 713.  
**FEATURES** Location/Qualifiers  
**source** 1..887  
 /organism="Reticuloendotheliosis virus"  
 /mol\_type="genomic RNA"  
 /db\_xref="taxon:11636"  
 246..750  
 /note="3' LTR"  
 LTR 805..806  
 /note="cryptic intron splice donor site"  
 misc\_feature 805..806  
 /note="cryptic intron splice donor site"  
**ORIGIN** About 700 bp after segment 1.  
 Query Match 94.4%; Score 503; DB 14; Length 887;  
 Best Local Similarity 99.0%; Pred. No. 8.8e-14;  
 Matches 506; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 23 ATGTGGAGGAGAGCTCCGGGGGAAATAGCGCTGCTGCTAACTGCAATATTAGCTTCTG 82  
 DB 245 ATGTGGAGGAGAGCTCCGGGGGAAATAGCGCTGCTGCTAACTGCAATATTAGCTTCTG 304  
 QY 83 TAATCATGCTTGTGCTTACCGCCGCAATGTATATATTGCTGATATCATTTTC 142  
 DB 305 TAATCATGCTTGTGCTTACCGCCGCAATGTATATATTGCTGATATCATTTTC 364  
 QY 143 TCGGAATCGGCATCAAGAGAGGCTCAATAACCAATAAGGAATGTTGTGAAGCAA 202  
 DB 365 TCGGAATCGGCATCAAGAGAGGCTCAATAACCAATAAGGAATGTTGTGAAGCAA 424  
 QY 203 GCATCAGACCACTTGCACATCCATCAACGAAACAGAGATGAACTATCATCTGA 262  
 DB 425 GCATCAGACCACTTGCACATCCATCAACGAAACAGAGATGAACTATCATCTGA 484  
 QY 263 GCCAATGTTGTAAAGGCGAGATGCTATCTCCATAGAGGAATGTCAATGCAATCC 322  
 DB 485 GCCAATGTTGTAAAGGCGAGATGCTATCTCCATAGAGGAATGTCAATGCAATCC 544  
 QY 323 TGTAAAGGCGCTATATTAAGCAAGTGCATCTTGGCTGGGGTGGCGCTCACATTTG 382  
 DB 545 TGTAAAGGCGCTATATTAAGCAAGTGCATCTTGGCTGGGGTGGCGCTCACATTTG 604  
 QY 383 TGTACATGCGGCCAGATTGCAATCTGTATATAAAGCTTTTCTTATATCTTCAGAT 442  
 DB 605 TGTACATGCGGCCAGATTGCAATCTGTATATAAAGCTTTTCTTATATCTTCAGAT 664  
 QY 443 TGGCAGTGAAGAGATTTTGTGCGTGTGGCTGCTTACCTGGGTGGGTATGGGATC 502  
 DB 665 TGGCAGTGAAGAGATTTTGTGCGTGTGGCTGCTTACCTGGGTGGGTATGGGATC 724  
 QY 503 CGGACTGAATCCGTATATTGGTACACA 533  
 DB 725 CGGACTGAATCCGTATATTGGTATATA 755

**LOCUS** AY255632 745 bp DNA linear VRL 30-APR-2003  
**DEFINITION** Fowlpox virus TCP-B1en ORF201 gene, partial cds;  
 Reticuloendotheliosis virus remnant LTR, complete sequence, and protein kinase-like protein gene, partial cds.  
**ACCESSION** AY255632  
**VERSION** GI:30267693  
**KEYWORDS** Fowlpox virus  
**SOURCE** Fowlpox virus  
**ORGANISM** Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Avipoxvirus.  
**REFERENCE** 1 (bases 1 to 745)  
**AUTHORS** Singh,P., Kim,T.-J. and Tripathy,D.N.  
**TITLE** Re-emerging fowlpox: evaluation of isolates from vaccinated flocks  
**JOURNAL** Avian Pathol. 29, 449-455 (2000)  
**REFERENCE** 2 (bases 1 to 745)  
**AUTHORS** Singh,P., Schmitzlein,W.M. and Tripathy,D.N.  
**TITLE** Reticuloendotheliosis Virus Sequences within the Genomes of Field Strains of Fowlpox Virus Display Variability  
**JOURNAL** J. Virol. (2003) In press  
**REFERENCE** 3 (bases 1 to 745)  
**AUTHORS** Singh,P., Schmitzlein,W.M. and Tripathy,D.N.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (13-MAR-2003) Veterinary Pathobiology, University of Illinois at Urbana-Champaign, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA  
**FEATURES** Location/Qualifiers  
**source** 1..745  
 /organism="Fowlpox virus"  
 /mol\_type="genomic DNA"  
 /strain="vaccine strain TCP-B1en"  
 /db\_xref="taxon:10261"  
 /note="from CEVA Laboratory, Overland Park, KS identical to sequence in the vaccine strain 'Chick VI Pox' (Vineyard Laboratories, Vineyard, NY)"  
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 /note="hypothetical protein; ORF1"  
 /codon\_start=1  
 /evidence=not experimental  
 /product="ORF201"  
 /protein\_id="AAP21482.1"  
 /db\_xref="GI:30267694"  
 /translation="NNDTSLPVAVKVIYGVTRI"  
 65..572  
 /note="Reticuloendotheliosis virus proviral remnant LTR"  
 643..>745  
 /note="ORF203; ORF2"  
 /codon\_start=1  
 /product="protein kinase-like protein"  
 /protein\_id="AAP21483.1"  
 /db\_xref="GI:30267695"  
 /translation="MDITWTWTFDIQFNDIPNIPYVDIEKPLIVISC"  
**ORIGIN**  
 Query Match 92.1%; Score 490.8; DB 14; Length 745;  
 Best Local Similarity 99.4%; Pred. No. 5.1e-140;  
 Matches 503; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 QY 28 GAGAGAGCTCGGGGGGAAATAGCGTGGCTGCTAATCCATATTAGCTTCTGTAATC 87  
 DB 68 GAGAGAGCTCGGGGGGAAATAGCGTGGCTGCTAATCCATATTAGCTTCTGTAATC 127  
 QY 88 ATGCTTGTGCTTACCGCCGCAATGTGATCTTGAATATTTCGCTGAAATCATTTCTCGGA 147  
 DB 128 ATGCTTGTGCTTACCGCCGCAATGTGATCTTGAATATTTCGCTGAAATCATTTCTCGGA 187  
 QY 148 ATCGGCAATCAAGAGAGGCTCATTAACCAATAAGGAATGTTGTGAAGCAAGCATC 207  
 DB 188 ATCGGCAATCAAGAGAGGCTCATTAACCAATAAGGAATGTTGTGAAGCAAGCATC 247  
 QY 208 AGACCACTTGACCATCAATCAAGAAACAAACAGAGATGAACTATCATCTGAGCCAA 267  
 DB 248 AGACCACTTGACCATCAATCAAGAAACAAACAGAGATGAACTATCATCTGAGCCAA 307

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QY 268 TGGTGTAAAGGAGATGATCTATCTCCAAATGAGGAAATGTCATGCAACATCTGTAA 327
Db 308 TGGTGTAAAGGAGATGATCTATCTCCAAATGAGGAAATGTCATGCAACATCTGTAA 367
QY 328 GGGCTATATTAAGCCAGATGATCTTGTCTCGGGGTGCGGCTCTACACATGTTGTGA 387
Db 368 GGGCTATATTAAGCCAGATGATCTTGTCTCGGGGTGCGGCTCTACACATGTTGTGA 427
QY 388 GGTGCGGCCAGATTCGAATCTGTAAATAAAGCTTTTCTTCTATATCTCGATTTGGA 447
Db 428 GGTGCGGCCAGATTCGAATCTGTAAATAAAGCTTTTCTTCTATATCTCGATTTGGA 487
QY 448 GTGAGAGAGATTTTGTCTGTGTGTGTGCTGCTGCTACTGAGGAGGATTCGAC 507
Db 488 GTGAGAGAGATTTTGTCTGTGTGTGTGCTGCTGCTACTGAGGAGGATTCGAC 547
QY 508 TGAATCGGTAGTATTCCTGATACACA 533
Db 548 TGAAT-CGTCTGATGTTGGATACACA 572
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RESULT 7
LOCUS A83548 940 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 1 from Patent WO9849334.
ACCESSION A83548
VERSION A83548.1 GI:6732807
SOURCE Reticuloendotheliosis virus
ORGANISM Reticuloendotheliosis virus
REFERENCE 1 (bases 1 to 940)
AUTHORS Gabus-Darlix C. and Darlix J.
TITLE NOVEL INTERNAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING SAME
JOURNAL Patent: WO 9849334-A 1 05-NOV-1998;
GABUS DARLIX CAROLINE (FR); INST NAT SANTE RECH MED (FR)
FEATURES
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        1..940
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            /mol_type="unassigned DNA"
            /strain="TYPE A (REV-A)"
            /isolate="LEADER 5' DE L'ARN GENOMIQUE REV-A"
            /db_xref="taxon:11636"
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## ORIGIN

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Query Match 82.4%; Score 439.4; DB 6; Length 940;
Best Local Similarity 93.3%; Pred. No. 3.8e-124;
Matches 501; Conservative 0; Mismatches 11; Indels 25; Gaps 3;

QY 22 AATGTGGAGGAGCTCCGGGGGAAATAGCGCTGCTCGCTAATGCAATTTAGCTTCT 81
Db 1 AATGTGGAGGAGCTCCGGGGGAAATAGCGCTGCTCGCTAATGCAATTTAGCTTCT 60
QY 82 GTAATCATGCTTGCTTGCCTTACCGCCCATGTACTGTATATATTTTGGCTGAT----- 134
Db 61 GTAATCATGCTTGCTTGCCTTACCGCCCATGTACTGTATATATTTTGGCTGATTTT 120
QY 135 -----ATCATTTCTCGAATCGGCATCAAGACAGGCTCATTAACCAATAAAG 182
Db 121 CTGCGAATCGGCATCAATTTCTCGAATCGGCATCAAGACAGGCTCATTAACCAATAAAG 180
QY 183 GAAATGTTTGTGAAGGCAAGCATCAAGCACTTGACCATCAAGCAAAACAG 242
Db 181 GAAATGTTTGTGAAGGCAAGCATCAAGCACTTGACCATCAAGCAAAACAG 240
QY 243 AAGTCGAATCATATCTAGGCAATGTTTGAAGGGGAGATGCTATCTCCATGAG 302
Db 241 AAGTCGAATCATATCTAGGCAATGTTTGAAGGGGAGATGCTATCTCCATGAG 300
QY 303 GAAATGTCATGCACA-----TCTGTGAAGGGGCTATATTAAGCAGGTGATCTTGC 357
Db 301 GAAATGTCATGCACACTCTGTCTGTGAAGGGGCTATATTAAGCAGGTGATCTTGC 360
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QY 358 TCGGGGTGCGGCTCTACATTTGTTGTACGTGCGGCCCAAGATTCGAATCTGTAAATAA 417
Db 361 TCGGGGTGCGGCTCTACATTTGTTGTACGTGCGGCCCAAGATTCGAATCTGTAAATAA 420
QY 418 AG-CTTTTCTTCTATATCTTCAGATTTGAGAGGAGGATTTTGTTCGTGCTTGG 476
Db 421 AGTTTCTTCTTCTATATCTTCAGATTTGAGAGGAGGATTTTGTTCGTGCTTGG 480
QY 477 CTGGCTACTAGGTTGGGATGAGATTCGGAATCGGATGATTTTCCGTACACA 533
Db 481 CTGGCTACTAGGTTGGGATGAGATTCGGAATCGGATGATTTTCCGTACACA 537
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RESULT 8
LOCUS BD006232 940 bp RNA linear PAT 31-JAN-2002
DEFINITION Novel internal ribosome entry site and vector containing same.
ACCESSION BD006232
VERSION BD006232.1 GI:18634603
KEYWORDS JP 2001500021-A/1.
SOURCE Reticuloendotheliosis virus
ORGANISM Reticuloendotheliosis virus
REFERENCE 1 (bases 1 to 940)
AUTHORS Lastre,M.L., Darlix,C.G. and Darlix,J.L.
TITLE Novel internal ribosome entry site and vector containing same
JOURNAL Patent: JP 2001500021-A 1 09-JAN-2001;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
OS Reticuloendotheliosis virus
PN JP 2001500021-A/1
PD 09-JAN-2001
PF 28-APR-1998 JP 1998546672
PR 28-APR-1997 FR 97/05203
PT MARCELO LOPEZ LASTRA,CAROLINE GABUS DARLIX,JEAN LUC DARLIX PC
C12N15/86,C12N15/11//C12N15/67
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source 1..940
    Location/Qualifiers
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            /organism="Reticuloendotheliosis virus".
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source
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## ORIGIN

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Query Match 82.4%; Score 439.4; DB 6; Length 940;
Best Local Similarity 93.3%; Pred. No. 3.8e-124;
Matches 501; Conservative 0; Mismatches 11; Indels 25; Gaps 3;

QY 22 AATGTGGAGGAGCTCCGGGGGAAATAGCGCTGCTCGCTAATGCAATTTAGCTTCT 81
Db 1 AATGTGGAGGAGCTCCGGGGGAAATAGCGCTGCTCGCTAATGCAATTTAGCTTCT 60
QY 82 GTAATCATGCTTGCTTGCCTTACCGCCCATGTACTGTATATATTTTGGCTGAT----- 134
Db 61 GTAATCATGCTTGCTTGCCTTACCGCCCATGTACTGTATATATTTTGGCTGATTTT 120
QY 135 -----ATCATTTCTCGAATCGGCATCAAGACAGGCTCATTAACCAATAAAG 182
Db 121 CTGCGAATCGGCATCAATTTCTCGAATCGGCATCAAGACAGGCTCATTAACCAATAAAG 180
QY 183 GAAATGTTTGTGAAGGCAAGCATCAAGCACTTGACCATCAAGCAAAACAG 242
Db 181 GAAATGTTTGTGAAGGCAAGCATCAAGCACTTGACCATCAAGCAAAACAG 240
QY 243 AAGTCGAATCATATCTAGGCAATGTTTGAAGGGGAGATGCTATCTCCATGAG 302
Db 241 AAGTCGAATCATATCTAGGCAATGTTTGAAGGGGAGATGCTATCTCCATGAG 300
QY 303 GAAATGTCATGCACA-----TCTGTGAAGGGGCTATATTAAGCAGGTGATCTTGC 357
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Db      301 GAAAGTCAATGCAACATCTGTCCTGTAGCGGCTATATAGCAGGTGCATCTTGC 360
Qy      358 TCGGGGCGCCGCTTACACATATGTTGTACGCGCCGCAAGTGAATCTGTAATAA 417
Db      361 TCGGGGCGCCGCTTACACATATGTTGTACGCGCCGCAAGTGAATCTGTAATAA 420
Qy      418 AG--CTTTTCTTCTATATCTTCAAGATTGACAGTGAAGAGATTGTTGTGTTGG 476
Db      421 AGTTTTTTCTTCTATATCTTCAAGATTGACAGTGAAGAGATTGTTGTGTTGG 480
Qy      477 CTGGCTACTGGGTGGGTAGGATCCGACTGAATCCGATATTTTGGTACACA 533
Db      481 CTGGCTACTGGGTGGGTAGGATCCGACTGAATCCGATATTTTGGTACACA 537

RESULT 9
LOCUS   S70398          545 bp      RNA      linear      VRL 23-SEP-1994
DEFINITION (LTR, U3, R and U5 regions, long terminal repeats, provirus)
[reticuloendotheliosis virus A REV-A, A, Genomic RNA, 545 nt].
ACCESSION S70398
VERSION   S70398.1 GI:547134
KEYWORDS Reticuloendotheliosis virus
SOURCE    Reticuloendotheliosis virus
ORGANISM  Viruses; Retroviridae; Gammaretrovirus.
REFERENCE 1 (bases 1 to 545)
AUTHORS   Filardo, E.J., Lee, M.F. and Humphries, E.H.
TITLES    Structural genes, not the LTRs, are the primary determinants of
JOURNAL   reticuloendotheliosis virus A-induced runting and bursal atrophy
MEDLINE   virology 202 (1), 116-128 (1994)
PUBMED    94279132
REMARK    Genbank staff at the National Library of Medicine created this
          entry [NCBI gi547132.1] from the original journal article.
          This sequence comes from Fig. 3.
FEATURES
  source          1..545
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                  /mol_type="genomic RNA"
                  /db_xref="taxon:11636"

ORIGIN
Query Match      82.3%; Score 438.4; DB 14; Length 545;
Best Local Similarity 93.1%; Pred. No. 7.6e-124;
Matches 501; Conservative 0; Mismatches 11; Indels 26; Gaps 3;

Qy      22 AATGTGGAGAGAGCTCCGGGGGAATAGGCTGCTCGCTAATCTGCATATTAGCTTCT 81
Db      1 AATGTGGAGAGAGCTCCGGGGGAATAGGCTGCTCGCTAATCTGCATATTAGCTTCT 60
Qy      82 GTAATCATGCTTGCTGCTTACCGCCGCAATGTATCTTGAATATTTGCTGAT----- 134
Db      61 GTAATCATGCTTGCTGCTTACCGCCGCAATGTATCTTGAATATTTGCTGATATTCT 120
Qy      135 -----ATCATTTCTCGGAATCGGCTAATAAGAGAGCTCTAATTAAG 182
Db      121 CTGGGAATCGGCAATTTCTCGGAATCGGCTAATAAGAGAGCTCTAATTAAG 180
Qy      183 GAAATGTTTGTGAAGGACATCAGACCACTTGACCATCCATCAGCAACAAACAG 242
Db      181 GAAATGTTTGTGAAGGACATCAGACCACTTGACCATCCATCAGCAACAAACAG 240
Qy      243 AGATCGAATCATATCTGAGCCAAATGTTGTAAAGGAGAGATCTATCTCAATGAG 302
Db      241 AGATCGAATCATATCTGAGCCAAATGTTGTAAAGGAGAGATCTATCTCAATGAG 300
Qy      303 GAAATGTCATGCAAC-----TCCTGTAAAGCGCTATATTAAGCAGTGCATCTTGC 357
Db      301 GAAATGTCATGCAACCTCTGTCGTAAAGCGCTATATTAAGCAGTGCATCTTGC 360
Qy      358 TCGGGGCGCCGCTTACACATATGTTGTACGTCGCGCCGCAAGTTCGAATCTGTAATAA 417

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Db      361 TCGGGGCGCCGCTTACACATATGTTGTACGCGCCGCAAGTGAATCTGTAATAA 420
Qy      418 AG--CTTTTCTTCTATATCTTCAAGATTGACAGTGAAGAGATTGTTGTGTTGG 475
Db      421 AGTTTTTTCTTCTATATCTTCAAGATTGACAGTGAAGAGATTGTTGTGTTGG 480
Qy      476 GCTGGCTACTGGGTGGGTAGGATCCGACTGAATCCGATATTTTGGTACACA 533
Db      481 GCTGGCTACTGGGTGGGTAGGATCCGACTGAATCCGATATTTTGGTACACA 538

RESULT 10
LOCUS   S79845          583 bp      DNA      linear      VRL 07-MAY-1993
DEFINITION (REV LTR) [Marek disease virus, attenuated strain JM-H13,
[reticuloendotheliosis virus insertion, insertion, 583 nt].
ACCESSION S79845
VERSION   S79845.1 GI:244514
KEYWORDS Gallid herpesvirus 2
SOURCE    Gallid herpesvirus 2
ORGANISM  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
          Alphaherpesvirinae; Marek's disease-like viruses.
REFERENCE 1 (bases 1 to 583)
AUTHORS   Iefort, R., Jones, D., Kost, R., Witter, R. and Kung, H.J.
TITLES    Retrovirus insertion into herpesvirus in vitro and in vivo
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (3), 991-995 (1992)
MEDLINE   92141243
PUBMED    1310544
REMARK    Genbank staff at the National Library of Medicine created this
          entry [NCBI gi547132.1] from the original journal article.
          This sequence comes from Fig 1C.
FEATURES
  source          1..583
                  /organism="Gallid herpesvirus 2"
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ORIGIN
Query Match      80.5%; Score 429; DB 14; Length 583;
Best Local Similarity 93.1%; Pred. No. 6.1e-121;
Matches 501; Conservative 0; Mismatches 11; Indels 26; Gaps 4;

Qy      22 AATGTGGAGAGAGCTCCGGGGGAATAGGCTGCTCGCTAATCTGCATATTAGCTTCT 81
Db      563 AATGTGGAGAGAGCTCCGGGGGAATAGGCTGCTCGCTAATCTGCATATTAGCTTCT 504
Qy      82 GTAATCATGCTTGCTGCTTACCGCCGCAATGTATCTTGAATATTTGCTGAT----- 134
Db      503 GTAATCATGCTTGCTGCTTACCGCCGCAATGTATCTTGAATATTTGCTGATATTCT 444
Qy      135 -----ATCATTTCTCGGAATCGGCTAATAAGAGAGCTCTAATTAAG 182
Db      443 CTGGGAATCGGCAATTTCTCGGAATCGGCTAATAAGAGAGCTCTAATTAAG 384
Qy      183 GAAATGTTTGTGAAGGACATCAGACCACTTGACCATCCATCAGCAACAAACAG 242
Db      383 GAAATGTTTGTGAAGGACATCAGACCACTTGACCATCCATCAGCAACAAACAG 324
Qy      243 AGATCGAATCATATCTGAGCCAAATGTTGTAAAGGAGAGATCTATCTCAATGAG 302
Db      323 AGATCGAATCATATCTGAGCCAAATGTTGTAAAGGAGAGATCTATCTCAATGAG 264
Qy      303 GAAATGTCATGCAAC-----TCCTGTAAAGCGCTATATTAAGCAGTGCATCTTGC 357
Db      263 GAAATGTCATGCAACCTCTGTCGTAAAGCGCTATATTAAGCAGTGCATCTTGC 204
Qy      358 TCGGGGCGCCGCTTACACATATGTTGTACGTCGCGCCGCAAGTTCGAATCTGTAATAA 417
Db      203 TCGGGGCGCCGCTTACACATATGTTGTACGTCGCGCCGCAAGTTCGAATCTGTAATAA 144

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QY 418 ACCTTTT-CTTCATATCTCAGATGGACGTAGAGAGA-ITTTGTTCTGTGTTG 475  
Db 143 ATTTTTCCTCTATATCTCAGATTTGGCAGTAGAGAGATTGTTGTCGTGCTAG 84  
QY 476 GCTGGCTACCTGGGTTAGGGATCCGACCTGAATCCGTATTTCCGTACACA 533  
Db 83 GCTGGCTACCTGGGTTAGGGATCCGACCTGAATCCGTATTTCTGTACACA 26

RESULT 11  
REXX2 859 bp DNA linear VRL 06-APR-1993  
LOCUS Spleen necrosis virus (3' end) integrated in chicken cell.  
DEFINITION V01205 J02389  
ACCESSION V01205.1 GI:61794  
VERSION  
KEYWORDS  
SOURCE Spleen necrosis virus  
ORGANISM Spleen necrosis virus  
VIRUSES; Retroid viruses; Retroviridae; Mammalian type C  
retroviruses; 1-Mammalian type C virus group.  
REFERENCE 1 (bases 1 to 859)  
AUTHORS Shimotohno,K., Mizutani,S. and Temin,H.M.  
TITLE Sequence of retrovirus provirus resembles that of bacterial  
transposable elements  
JOURNAL Nature 285 (5766), 550-554 (1980)  
MEDLINE 80254544  
PUBMED 6250038  
FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:11836"  
source <1..740  
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/proviral  
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/db\_xref="taxon:11836"  
741..>859  
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/note="cellular DNA"

ORIGIN  
Query Match 58.9%; Score 313.8; DB 14; Length 859;  
Best Local Similarity 85.3%; Pred. No. 2.3e-85;  
Matches 424; Conservative 0; Mismatches 57; Indels 16; Gaps 6;

QY 52 GCTGGCTCGCTACCTGCATATTTAGCTTCTGTATCATGCTTGCCTTAGCCGCAT 111  
Db 235 GCTGGCTCGCTACCTGCATATTTAGCTTCTGTATCATGCTTGCCTTAGCCGCAT 294  
QY 112 TGTACTGTATAT--ATTTCGTGATATCATTTCTCGAATCGGCATCAAGTTTCGTTCTCGAGGCAAGCC 354  
Db 295 TGTACTGTATATGCAATTTCTCGAATCGGCATCAAGTTTCGTTCTCGAGGCAAGCC 354  
QY 169 ATAAACCAATAAAGGAATGTTTGTGAAGGCAAGCATCAGCACTTGCAACCATCAAT 228  
Db 355 ACAACCAATAAAGGAAGCGCAGCAAGGCAAGCATCAGCACTTGCGCCATCCAT 414  
QY 229 CACGAACAAACAGAGATGGAATCATCACT--GAGCCAATGGTGTAAAGGCGAGATGC 287  
Db 415 CATGAACGAGACAGAGATCGACTATCATCTGAGCCCAATGGTGTAAAGGCGAGATGC 474  
QY 288 TATCTCCAAATGAGGGAATATGTCATGCAATC-----CTGTAAAGCGCTATATAAG 340  
Db 475 TACTCTCAATGAGGGAATATGTCATGTAACACCTGTAACTGTAAAGCGCTATATAAG 534  
QY 341 CCAAGTGATCTCTTGTCTCGGGTGCCTTACACA---TTGTTGAGAGTGCAGCC 397  
Db 535 CCGGGTACATCTCTTGTCTCGGGTGCCTTGTGATGTTGTTGAGAGTGCAGCC 594  
QY 398 ACATTGATCTGTATATAAAGCTTTTCTTCTATATCTCAGATGGACGTAGAGAG 457

Db 595 AGATTCCGATCTGTATAA--CTTTTCTTCAATCCACATTTGGCAGTAGAGAG 653  
QY 458 ATTTGTTCTGTGTTGTTGCTGCTACTGGTGGG--GTAGGGATCCGATCAATCCGT 516  
Db 654 ATTTGTTCTGTGTTGTTGCTGCTACTGGTGGG--GTAGGGATCCGATCAATCCGT 713  
QY 517 AGTATTTCCGTACACA 533  
Db 714 AGTACTTCGTACACA 730

RESULT 12  
REXX1 891 bp DNA linear VRL 29-APR-2000  
LOCUS Spleen necrosis virus (5' end) integrated in chicken cell.  
DEFINITION V01204 J02388 M12296  
ACCESSION V01204.1 GI:61793  
VERSION  
KEYWORDS  
SOURCE Spleen necrosis virus  
ORGANISM Spleen necrosis virus  
VIRUSES; Retroid viruses; Retroviridae; Mammalian type C  
retroviruses; 1-Mammalian type C virus group.  
REFERENCE 1 (bases 1 to 891)  
AUTHORS Shimotohno,K., Mizutani,S. and Temin,H.M.  
TITLE Sequence of retrovirus provirus resembles that of bacterial  
transposable elements  
JOURNAL Nature 285 (5766), 550-554 (1980)  
MEDLINE 80254544  
PUBMED 6250038  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 58.9%; Score 313.8; DB 14; Length 891;  
Best Local Similarity 85.3%; Pred. No. 2.3e-85;  
Matches 424; Conservative 0; Mismatches 57; Indels 16; Gaps 6;

QY 52 GCTGGCTCGCTACCTGCATATTTAGCTTCTGTATCATGCTTGCCTTAGCCGCAT 111  
Db 99 GCTGGCTCGCTACCTGCATATTTAGCTTCTGTATCATGCTTGCCTTAGCCGCAT 158  
QY 112 TGTACTGTATAT--ATTTCGTGATATCATTTCTCGAATCGGCATCAAGTTTCGTTCTCGAGGCAAGCC 168  
Db 159 TGTACTGTATATGCAATTTCTCGAATCGGCATCAAGTTTCGTTCTCGAGGCAAGCC 218  
QY 169 ATAAACCAATAAAGGAATGTTTGTGAAGGCAAGCATCAGCACTTGCAACCATCAAT 228  
Db 219 ACAACCAATAAAGGAAGCGCAGCAAGGCAAGCATCAGCACTTGCGCCATCCAT 278  
QY 229 CACGAACAAACAGAGATGGAATCATCACT--GAGCCAATGGTGTAAAGGCGAGATGC 287  
Db 279 CATGAACGAGACAGAGATCGACTATCATCTGAGCCCAATGGTGTAAAGGCGAGATGC 338  
QY 288 TATCTCCAAATGAGGGAATATGTCATGCAATC-----CTGTAAAGCGCTATATAAG 340  
Db 339 TACTCTCAATGAGGGAATATGTCATGTAACACCTGTAACTGTAAAGCGCTATATAAG 398  
QY 341 CCAAGTGATCTCTTGTCTCGGGTGCCTTACACA---TTGTTGAGAGTGCAGCC 397



Db 399 CCGGATCATCTCTGCTCGGGGTCCGCTCGACATTTGTTGAGCGTCCGCC 458  
 QY 398 AGATGCAATCTGTAATAAAGCTTTTCTTATATCTCAGATTGGACAGAGAG 457  
 Db 459 AGATTGCAATCTGTAATAAAGCTTTTCTTATATCTCAGATTGGACAGAGAG 517  
 QY 458 ATTTTGTCTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 516  
 Db 518 ATTTTGTCTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 577  
 QY 517 AGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 577  
 Db 578 AGTACTTCGGTACACA 594

RESULT 13  
 AF006066 1022 bp DNA linear VRL 16-SEP-1997  
 LOCUS Fowlpox virus S envelope glycoprotein (env) gene, partial cds and  
 DEFINITION 3' long terminal repeat, complete sequence.  
 ACCESSION AF006066  
 VERSION AF006066.1 GI:2393896  
 KEYWORDS Fowlpox virus  
 SOURCE Fowlpox virus  
 ORGANISM Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

REFERENCE 1 (bases 1 to 1022)  
 AUTHORS Hertig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.  
 TITLE Field and vaccine strains of fowlpox virus carry integrated  
 JOURNAL sequences from the avian retrovirus, reticuloendotheliosis virus  
 MEDLINE virology 235 (2), 367-376 (1997)  
 PUBMED 97428585

REFERENCE 2 (bases 1 to 1022)  
 AUTHORS Hertig,C.H., Coupar,B.E.H., Gould,A.R. and Boyle,D.B.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-MAY-1997) Division of Animal Health, CSIRO, 5  
 Portarlington Road, Geelong, Victoria 3213, Australia

FEATURES  
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 /strain="S (Standard Vaccine strain)"  
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 Ltd, Castle Hill, New South Wales, Australia  
 integrated reticuloendotheliosis virus"  
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 409..679  
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 been duplicated."  
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CDS

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 /note="ORF1"  
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 DNPVSLKFTCPKNSIRQPIKELDLRLSLSSESHVIKLYGYILD"

ORIGIN

Query Match 38.7%; Score 206.4; DB 14; Length 1022;  
 Best Local Similarity 99.1%; Pred. No.3.3e-52;  
 Matches 218; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 1 TGTGGAGGAGAGCTCCGGGGGAATGTGGAGGAGAGCTCCGGGGGAATACCGTGGCTCG 60  
 Db 409 TGTGGAGGAGAGCTCCGGGGGAATGTGGAGGAGAGCTCCGGGGGAATACCGTGGCTCG 467  
 QY 61 CTAACTGCCATATTAAGCTTCTGATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 Db 468 CTAACTGCCATATTAAGCTTCTGATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 527  
 QY 121 TATATTTGCTGATATCATATTTCTGATATCGATGAGCATGAGAGGCTCATTAACATTA 180  
 Db 528 TATATTTGCTGATATCATATTTCTGATATCGATGAGCATGAGAGGCTCATTAACATTA 587  
 QY 181 AGAAATGTTTGTGTAAGGACAGATCAGACCTTGCCAC 220  
 Db 588 AGAAATGTTTGTGTAAGGACAGATCAGACCTTGCCAC 627

RESULT 14  
 AY255633 485 bp DNA linear VRL 30-APR-2003  
 LOCUS Fowlpox virus 'Chick-n-Pox' ORF201 gene, partial cds;  
 DEFINITION Reticuloendotheliosis virus remnant LTR, complete sequence; and  
 ACCESSION AY255633  
 VERSION AY255633.1 GI:30267696  
 KEYWORDS Fowlpox virus  
 SOURCE Fowlpox virus  
 ORGANISM Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

REFERENCE 1 (bases 1 to 485)  
 AUTHORS Singh,P., Kim,T.-U. and Tripathy,D.N.  
 TITLE Re-emerging fowlpox: evaluation of isolates from vaccinated flocks  
 JOURNAL Avian Pathol. 29, 449-455 (2000)  
 REFERENCE 2 (bases 1 to 485)  
 AUTHORS Singh,P., Schmitzlein,W.M. and Tripathy,D.N.  
 TITLE Reticuloendotheliosis Virus Sequences within the Genomes of Field  
 JOURNAL Strains of Fowlpox Virus Display Variability  
 J. Virol. (2003) In press

REFERENCE 3 (bases 1 to 485)  
 AUTHORS Singh,P., Schmitzlein,W.M. and Tripathy,D.N.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-MAR-2003) Veterinary Pathobiology, University of  
 Illinois at Urbana-Champaign, 2001 S. Lincoln Avenue, Urbana, IL  
 61802, USA

FEATURES  
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 /organism="Fowlpox virus"  
 /mol\_type="genomic DNA"  
 /strain="vaccine strain 'Chick-n-Pox'"  
 /db\_xref="taxon:10261"  
 /note="from Fort Dodge Animal Health, Fort Dodge, IA  
 identical sequence also found in strains pp-VRC (Intervet,  
 Inc., Millsboro, DE), Fowlpox (Mallinckrodt Veterinary,  
 Inc., Millsboro, DE), Pigeonpox (Intervet, Inc., Millsboro, DE),  
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 Omaha, NE and Select Laboratories, Gainesville, GA"  
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 /note="hypothetical protein; ORF1"  
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 /db\_xref="GI:30267697"  
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 383..>485

CDS

misc\_feature  
 CDS

/note="ORF203; ORF2"  
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Best Local Similarity 100.0%; Pred. No. 4,3e-48;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGAGGAGCTCCGGGGGGAATAGCGCTGCTCGCTAACTGCAATTAAGCTTCTGTAATC 87  
DB 68 GGAGGAGCTCCGGGGGGAATAGCGCTGCTCGCTAACTGCAATTAAGCTTCTGTAATC 127  
QY 88 ATGCTTGCTTGCTTGAAGCGGCTGCTGTAATTAATTTGCTGATATCTTCGGA 147  
DB 128 ATGCTTGCTTGCTTGAAGCGGCTGCTGTAATTAATTTGCTGATATCTTCGGA 187  
QY 148 ATGCGCATCAAGAGCGGCTCATTAACATTAAGAAATGTTGTTGAAGCAAGCATC 207  
DB 188 ATGCGCATCAAGAGCGGCTCATTAACATTAAGAAATGTTGTTGAAGCAAGCATC 247  
QY 208 AGACCACTTGAC 220  
DB 248 AGACCACTTGAC 260

## ORIGIN

Query Match 36.2%; Score 193; DB 14; Length 2640;  
Best Local Similarity 100.0%; Pred. No. 4.7e-48;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGAGGAGCTCCGGGGGGAATAGCGCTGCTCGCTAACTGCAATTAAGCTTCTGTAATC 87  
DB 908 GGAGGAGCTCCGGGGGGAATAGCGCTGCTCGCTAACTGCAATTAAGCTTCTGTAATC 967  
QY 88 ATGCTTGCTTGCTTGAAGCGGCTGCTGTAATTAATTTGCTGATATCTTCGGA 147  
DB 968 ATGCTTGCTTGCTTGAAGCGGCTGCTGTAATTAATTTGCTGATATCTTCGGA 1027  
QY 148 ATGCGCATCAAGAGCGGCTCATTAACATTAAGAAATGTTGTTGAAGCAAGCATC 207  
DB 1028 ATGCGCATCAAGAGCGGCTCATTAACATTAAGAAATGTTGTTGAAGCAAGCATC 1087  
QY 208 AGACCACTTGAC 220  
DB 1088 AGACCACTTGAC 1100

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Job time : 2254 secs

## FEATURES

source

## CDS

/organism="Fowlpox virus"  
/mol\_type="genomic DNA"  
/strain="W (mild vaccine strain)"  
/db\_xref="taxon:10261"  
/note="mild vaccine strain from Cyanamid-Webster Pty Ltd, Castle Hill, New South Wales, Australia.  
Part 1 A' fragment  
integrated reticuloendotheliosis virus"  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 00:25:56 ; Search time 351 Seconds  
(without alignments)  
6450.967 Million cell updates/sec

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Perfect score: 533  
Sequence: 1 tgcgggagggagctccggggg.....cgtgatttcggtacacaa 533

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506.8	95.1	512	2	AAK26109 Chicken s
2	506	94.9	536	2	AAK26110 Fowlpox v
3	506	94.9	4643	2	AAK26113 Fowlpox v
4	439.4	82.4	940	2	AAV63778 Sequence
5	206.4	38.7	296	2	AAK26111 Fowlpox v
6	206.4	38.7	1022	2	AAK26115 Fowlpox v
7	193	36.2	298	2	AAK26112 Fowlpox v
8	193	36.2	1100	2	AAK26114 Fowlpox v
9	193	36.2	266145	9	ADBE87477 Fowlpox v
10	155	29.1	578	2	AAV63779 Sequence
11	145	27.2	3878	2	AAQ76041 Retrovitu
12	145	27.2	5528	2	AAQ76038 Retrovitu
13	134.6	25.3	5525	2	AAQ76039 Retrovitu
14	127.6	23.9	5519	2	AAQ76040 Retrovitu
15	33.8	6.3	714	4	AAK931988 Human gen
16	33.8	6.3	714	4	AAK931988 Human gen
17	33.8	6.3	2604	5	AAK931652 Human CDN
18	33.8	6.3	13079	5	AAK931652 Human CDN
19	33.8	6.3	25967	5	ABAI18638 Human ner
20	33.8	6.3	96960	7	ABAI18639 Human ner
21	33.8	6.3	96960	7	ABAI18639 Human ner
22	33.8	6.3	96960	9	ADB87938 Human UGT
23	33.8	6.3	96960	9	ADB87938 Human UGT
					ADB96921 Human MDR

24	33.8	6.3	96960	9	ADB92112 Human MDR
25	33.8	6.3	123785	7	ABX77171 DNA seque
26	33.4	6.3	2000	7	ADA71938 Rice gene
27	33.4	6.3	3824	9	ADBE63200 Human gen
28	33.4	6.3	3824	9	ADBE63196 Human gen
29	33.4	6.3	3824	9	ADBE63208 Human gen
30	33.4	6.3	3824	9	ADBE63204 Human gen
31	33.4	6.3	6617	4	AAI97964 Human gen
32	33.4	6.3	6617	8	ACA92322 Lawsonia
33	33.2	6.2	2000	7	ADA71938 Rice gene
34	33	6.2	557	6	ADBE61561 Human can
35	33	6.2	4703	3	AACT76621 Human ORF
36	33	6.2	110000	2	AAV21209 07 of
37	32.6	6.1	96595	8	ADA02726 Human SYK
38	32.6	6.1	96595	9	ADA02726 Human SYK
39	32.2	6.0	703	4	AAK92046 Human CDN
40	32.2	6.0	703	4	AAK93694 Human CDN
41	32.2	6.0	3388	7	AAK47154 Human nuc
42	32.2	6.0	3396	4	AAK94808 Human ful
43	32.2	6.0	3410	7	ABX70998 Novel hum
44	32.2	6.0	20346	8	ADB66951 E. coli K
45	32	6.0	9347	6	ABL49336 Human pol

#### ALIGNMENTS

RESULT 1  
AAK26109 standard; DNA; 512 BP.  
AC AAK26109;  
XX 17-OCT-2003 (revised)  
DT 20-MAY-1999 (first entry)  
XX  
DE Chicken syncytial virus provirus REV LTR sequence.  
XX  
KM Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;  
KM vaccine; chicken; LTR; long terminal repeat; ss.  
XX  
OS Reticuloendotheliosis virus.  
XX  
OS WO9907852-A1.  
XX  
PD 18-FEB-1999.  
XX  
PF 07-AUG-1998; 98MO-AU000628.  
XX  
PR 08-AUG-1997; 97AU-00008454.  
XX  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX  
PI Hertig C, Coupar BEH, Gould AR, Boyle DB;  
XX WPI; 1999-167428/14.  
XX  
XX Recombinant vaccine against fowlpox virus - is free of contamination from  
PT reticuloendotheliosis virus, used to prevent the virus occurrence in  
PT chickens.  
XX  
PS Example 4; Fig 5; 127pp; English.  
XX  
XX The invention relates to a recombinant fowlpox virus (FPV) whose nucleic  
XX acid does not encode an active reticuloendotheliosis virus (REV), and  
XX whose genome does not contain any REV sequence. The recombinant FPV is  
XX used to produce a vaccine against fowlpox virus. The vaccine is used to  
XX prevent the occurrence of fowlpox virus in chickens. The chickens can be  
XX vaccinated at older than 1 day of age. Alternatively, chickens older than  
XX 1 day can be vaccinated with the vaccine subsequent to vaccination with  
XX FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains  
XX of FPV carry integrated REV sequences. Some of the FPV strains carry a  
XX near full length provirus of REV, and can give rise to infectious REV

CC when transfected into cell cultures and when chickens are infected. The  
 CC present invention provides the means by which a FPV vaccine free from  
 CC contamination by REV may be produced. (Updated on 17-OCT-2003 to  
 CC standardise OS field)

XX  
 SQ Sequence 512 BP; 130 A; 113 C; 129 G; 140 T; 0 U; 0 Other;

Query Match 95.1%; Score 506.8; DB 2; Length 512;  
 Best Local Similarity 99.6%; Pred. No. 8.7e-162;  
 Matches 508; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 TGTGGAGAGGAGTCCGGGGGGAATAGCCCTGGCTGCTAATGCTCAATTAAGTTCTGT 83  
 DB 1 TGTGGAGAGGAGTCCGGGGGGAATAGCCCTGGCTGCTAATGCTCAATTAAGTTCTGT 60  
 QY 84 AATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 143  
 DB 61 AATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 QY 144 CGGAATCGGCATCAAGAGAGGCTCAATTAAGCAATTAAGCAATTAAGCAATTAAG 203  
 DB 121 CGGAATCGGCATCAAGAGAGGCTCAATTAAGCAATTAAGCAATTAAGCAATTAAG 180  
 QY 204 CATGAGACCATTTGACCATTCATCAAGAAACAGAGATGCAATTAATCAATTAAG 263  
 DB 181 CATGAGACCATTTGACCATTCATCAAGAAACAGAGATGCAATTAATCAATTAAG 240  
 QY 264 CCAATGCTTTGTAAGAGGAGATGCTATCTCCATGAGGAGAAATGTGATCAATCT 323  
 DB 241 CCAATGCTTTGTAAGAGGAGATGCTATCTCCATGAGGAGAAATGTGATCAATCT 300  
 QY 324 GTAACCGCTATTAAGAGGAGATGCTATCTCTGCTGCGGGTCCGCTCAACATTTGT 383  
 DB 301 GTAACCGCTATTAAGAGGAGATGCTATCTCTGCTGCGGGTCCGCTCAACATTTGT 360  
 QY 384 GTGAGTGGCGGCCAGATTCGATCTGATTAATTAAGCTTTCTTCTATATCCCAATTT 443  
 DB 361 GTGAGTGGCGGCCAGATTCGATCTGATTAATTAAGCTTTCTTCTATATCCCAATTT 420  
 QY 444 GGCAGTGAAGAGATTTTGTTCGTGATGTTGGCTGAGCTCACTGAGGAGGAGATTC 503  
 DB 421 GGCAGTGAAGAGATTTTGTTCGTGATGTTGGCTGAGCTCACTGAGGAGGAGATTC 480  
 QY 504 GGACTGAATCCGTATATTTGGGTACACA 533  
 DB 481 GGACTGAATCCGTATATTTGGGTACACA 510

RESULT 2  
 AAX26110  
 ID AAX26110 standard; DNA; 536 BP.

AC AAX26110;

DT 20-MAY-1999 (first entry)

DE Fowlpox virus (FPV M5) LTR sequence.

KM Fowlpox virus; FPV, recombinant; reticuloendotheliosis virus; REV;

KW vaccine; chicken; LTR; long terminal repeat; ss.

OS Fowlpox virus.

PN WO9907852-A1.

PD 18-FEB-1999.

PF 07-AUG-1998; 98WO-AU000628.

PR 08-AUG-1997; 97AU-00008454.

PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX

PI Hertig C, Coupar BEH, Gould AR, Boyle DB;  
 DR WPI; 1999-167428/14.  
 PT Recombinant vaccine against fowlpox virus - is free of contamination from  
 PT reticuloendotheliosis virus, used to prevent the virus occurrence in  
 PT chickens.

PS Claim 18; Fig 5; 127pp; English.

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic  
 CC acid does not encode an active reticuloendotheliosis virus (REV), and  
 CC whose genome does not contain any REV sequence. The recombinant FPV is  
 CC used to produce a vaccine against fowlpox virus. The vaccine is used to  
 CC prevent the occurrence of fowlpox virus in chickens. The chickens can be  
 CC vaccinated at older than 1 day of age. Alternatively, the chickens older than  
 CC 1 day can be vaccinated with the vaccine subsequent to vaccination with  
 CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains  
 CC of FPV carry integrated REV sequences. Some of the FPV strains carry a  
 CC near full length provirus of REV, and can give rise to infectious REV  
 CC when transfected into cell cultures and when chickens are infected. The  
 CC present invention provides the means by which a FPV vaccine free from  
 CC contamination by REV may be produced. Sequences AAX26110-115 represent  
 CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid  
 CC molecule can comprise a FPV LTR sequence selected from the above

SQ Sequence 536 BP; 145 A; 115 C; 133 G; 143 T; 0 U; 0 Other;

Query Match 94.9%; Score 506; DB 2; Length 536;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-161;  
 Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGAGGAGGCTCCGGGGGGAATAGCGCTGCTGCTAATGCTCAATTAAGTTCTGTAATC 87  
 DB 29 GGAGGAGGCTCCGGGGGGAATAGCGCTGCTGCTAATGCTCAATTAAGTTCTGTAATC 88  
 QY 88 ATGCTTGTGCTTATAGCCGATTTGATTAATTAATTAATTAATTAATTAATTAATTAAT 147  
 DB 89 ATGCTTGTGCTTATAGCCGATTTGATTAATTAATTAATTAATTAATTAATTAATTAAT 148  
 QY 148 ATGCGATTAAGAGGAGGCTCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTC 207  
 DB 149 ATGCGATTAAGAGGAGGCTCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTC 208  
 QY 208 AGACCACTTGACCAATCAATCAAGAAACAGAGATGCAATCAATCAATCAATCAATCAAT 267  
 DB 209 AGACCACTTGACCAATCAATCAAGAAACAGAGATGCAATCAATCAATCAATCAATCAAT 268  
 QY 268 TGTGTTAAAGGCGAGATGCTATCTCCATGAGGAGAAATGTCAATCAATCTGTA 327  
 DB 269 TGTGTTAAAGGCGAGATGCTATCTCCATGAGGAGAAATGTCAATCAATCTGTA 328  
 QY 328 GCGGCTATTAAGGCGAGATGCTATCTCCATGAGGAGAAATGTCAATCAATCTGTA 387  
 DB 329 GCGGCTATTAAGGCGAGATGCTATCTCCATGAGGAGAAATGTCAATCAATCTGTA 388  
 QY 388 CGTGGCGCCAGATTCGATCTGATTAATTAAGCTTTCTTCTATATCTGAGATTGGCA 447  
 DB 389 CGTGGCGCCAGATTCGATCTGATTAATTAAGCTTTCTTCTATATCTGAGATTGGCA 448  
 QY 448 GTGAGAGAGATTTTGTTCGTGATGTTGGCTGAGCTCACTGAGGAGGAGATCCGAGC 507  
 DB 449 GTGAGAGAGATTTTGTTCGTGATGTTGGCTGAGCTCACTGAGGAGGAGATCCGAGC 508  
 QY 508 TGAATCCGTATATTTGGGTACACA 533  
 DB 509 TGAATCCGTATATTTGGGTACACA 534

RESULT 3  
 AAX26113  
 ID AAX26113 standard; DNA; 4643 BP.

XX

AC	AAK26113;
XX	20-MAY-1999 (first entry)
DT	Fowlpox virus (FPV S) 5' LTR sequence.
XX	
DE	Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
KW	vaccine; chicken; LTR; long terminal repeat; ss.
XX	
OS	Fowlpox virus.
XX	
PN	M09907852-A1.
PD	18-FEB-1999.
XX	
PF	07-AUG-1998; 98MO-AU000628.
XX	
PR	08-AUG-1997; 97AU-00008454.
PA	(CSIR ) COMMONWEALTH SCI & IND RES ORG.
FL	Hertig C, Coupar BEH, Gould AR, Boyle DB;
DR	WPI; 1999-167428/14.
XX	
PT	Recombinant vaccine against fowlpox virus - is free of contamination from
PT	reticuloendotheliosis virus, used to prevent the virus occurrence in
FT	chickens.
XX	
PS	Claim 18; Fig 6; 127pb; English.
XX	
CC	The invention relates to a recombinant fowlpox virus (FPV) whose nucleic
CC	acid does not encode an active reticuloendotheliosis virus (REV), and
CC	whose genome does not contain any REV sequence. The recombinant FPV is
CC	used to produce a vaccine against fowlpox virus. The vaccine is used to
CC	prevent the occurrence of fowlpox virus in chickens. The chickens can be
CC	vaccinated at older than 1 day of age. Alternatively, chickens older than
CC	1 day can be vaccinated with the vaccine subsequent to vaccination with
CC	FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
CC	of FPV carry integrated REV sequences. Some of the FPV strains carry a
CC	near full length provirus of REV, and can give rise to infectious REV
CC	when transfectsed into cell cultures and when chickens are infected. The
CC	present invention provides the means by which a FPV vaccine free from
CC	contamination by REV may be produced. Sequences AAX26110-115 represent
CC	FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
CC	molecule can comprise a FPV LTR sequence selected from the above
XX	
SQ	Sequence 4643 BP; 1326 A; 1015 C; 1127 G; 1175 T; 0 U; 0 Other;
Query Match	94.9%; Score 506; DB 2; Length 4643;
Best Local Similarity	100.0%; Pred. No. 5,2e+61; Indels 0; Gaps 0;
Matches	506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dy	28 GGAGGGAGCTCGGGGGGAATAGCGCTGCCTACTGCATATTAGCTTGTATTC 87
Dd	1259 GGAGGGAGCTCGGGGGGAATAGCGCTGCCTACTGCATATTAGCTTGTATTC 1318
Dy	88 ATGCTGTGTTGCCCTTAAGCCGCACTTGATCTGATATATTTGGCGATATCATTTCTGGGA 147
Dd	1319 ATGCTGTGTTGCCCTTAAGCCGCACTTGATCTGATATATTTGGCGATATCATTTCTGGGA 1378
Dy	148 ATCGGCATCAGAAGAGGCTCATATAACCATTAAGAAATGTTTGTGAAGCAAGCATC 207
Dd	1379 ATCGGCATCAGAAGAGGCTCATATAACCATTAAGAAATGTTTGTGAAGCAAGCATC 1438
Dy	208 AGACCACCTTGACCATCATATCAGAACAAACAGAGATGCACTATCATACTGAGCCA 267
Dd	1439 AGACCACCTTGACCATCATATCAGAACAAACAGAGATGCACTATCATACTGAGCCA 1498
Dy	268 TGTTTTTAAAAGGGAGATGCTATCTCCAAATGAAGGAAAAATGTATGCAATCTCTGTAA 327
Dd	1499 TGTTTTTAAAAGGGAGATGCTATCTCCAAATGAAGGAAAAATGTATGCAATCTCTGTAA 1558

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OY 328 GGGGTATATATAGACAGATGATCTCTGTGCTGGGGGTCGCCGTCTTCAACATTGTGTGA 387
Db 1559 GGGGTATATATAGACAGATGATCTCTGTGCTGGGGGTCGCCGTCTTCAACATTGTGTGA 1618
OY 388 CGTGGGCGCCAGATTGCATCTGTATATAAAGCTTTTCTTCTATATCTTCAGATTGGCA 447
Db 1619 CGTGGGCGCCAGATTGCATCTGTATATAAAGCTTTTCTTCTATATCTTCAGATTGGCA 1678
OY 448 GTGAGAGAGATTTTGTTCGTGTGTGTGGCTGCGCTTACTGGGTGGGGTAGGGATCCGAC 507
Db 1679 GTGAGAGAGATTTTGTTCGTGTGTGTGGCTGCGCTTACTGGGTGGGGTAGGGATCCGAC 1738
OY 508 TGAATCCGTACTATTTGGGTACACA 533
Db 1739 TGAATCCGTACTATTTGGGTACACA 1764

RESULT 4
AAV63778
ID AAV63778 standard; DNA, 940 BP.
XX
XX AAV63778;
AC
XX
XX 17-MAR-1999 (first entry)
XX
XX
XX Sequence derived from the 5' end of REV-A.
DB
XX Reticuloendotheliosis virus type A; REV-A; 5' end genomic RNA;
XX type C retrovirus; internal ribosome entry site; IRES; encapsidation;
XX retroviral vector; gene therapy; ss.
XX
XX Reticuloendotheliosis virus.
OS
XX FR2762615-A1.
XX
XX 30-OCT-1998.
XX
XX 28-APR-1997; 97FR-00005203.
XX
XX 28-APR-1997; 97FR-00005203.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA
XX Lopez Lastrea M, Gabus Darlix C, Darlix JL;
PI
XX WPI, 1999-037487/04.
DR
XX
XX Expression vectors containing IRES and/or encapsidation enhancer -
PT derived from type C retrovirus other than FMLV and MoMLV.
XX
XX
XX Claim 5; Page 31-32; 43p; French.
XX
XX The present sequence is derived from the 5' end of the genomic RNA of
XX Reticuloendotheliosis virus type A (REV-A). The specification also
XX describes nucleotide sequence derived from all or part of the 5' end of
XX the genomic RNA of a type C retrovirus other than Friend murine leukemia
XX virus (FMLV) and MoJomly murine leukemia virus (MoMLV). The 5' derived
XX sequences are used as an internal ribosome entry site (IRES) in a vector
XX for permitting or enhancing the encapsidation of a retroviral vector. The
XX vectors can be used for gene therapy, production of recombinant
XX polypeptides or production of transgenic animals
XX
XX
XX Sequence 940 BP; 190 A; 225 C; 260 G; 0 T; 265 U; 0 Other;
SQ

Query Match 82.4%; Score 439.4; DB 2; Length 940;
Best Local Similarity 68.2%; Pred. No. 1.1e-138;
Matches 366; Conservative 135; Mismatches 11; Indels 25; Gaps 3;

OY 22 AATGTGGAGAGGAACTCCGGGGGGAAGAAGGCTGTGCTGTAATGCAATATTAAGCTTCT 81
Db 1 AATUGGGAGAGGAACTCCGGGGGGAANAAGGCTGCGCAATGCGCAUUAUUAAGCTUUC 60
OY 82 GTAATCATGCTGCTTGGCTTACCGCGCATTTGATCTGATATATTTGCTGAT----- 134

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Db      61  GUAAUCAGUCUGUCUGCCUUAACCCGCAUUGACUUGAUAUAUUUCUGUAUUCAUUU 120
Qy      135  -----ATCATTTCTCGGAATCGGCATCAAGACAGGCTCATTAACCAATTAAG 182
Db      121  CUGGAAUUCGGCAUUCUUUCUGGAUUCGGCAUCAAAGACAGGCGUCANAGACUAUAAAG 180
Qy      183  GAAATGTTTGTGGAAGCAAGCATCAGACCACTTGCACATCCATCCATCAGAACAAACAG 242
Db      181  GAAAUUUGCGUGGAGCGAGCAUACAGACCAUUCGCGCAUCCAAUACAAGCAAAACAG 240
Qy      243  AGATGCACTATCATCTAGCAAGCAATGCTTGAAGGCGAGATGCTATCTCCAAAGAG 302
Db      241  AGAUGCAACUACUACAUGAGCAUUGUGUAAAGGCGAUAUCCUCCAUUAGG 300
Qy      303  GAAATGTCATCAACA-----TCTCTAAGCGGCTATATAAGCAGAGTCATCTTTCG 357
Db      301  GAAAUUUGCAUACCAUCCUUGUCUUAAGCGCUAUAUAAGCAGAGUCACUUCUUCG 360
Qy      358  TCGGGGTGCGCGTCTCTAACAATTGTTGACGTGCGGCCAGATTCGATCTGTAATAA 417
Db      361  UCGGGGUCGCGGUCUACAUUUGUGAGCGCGGCCAGAUUUGGAUUCUGUAUAA 420
Qy      418  AG-CTTTTCTTCTATATCTCTAGATTGAGAGAGAGAGATTGTTGTGTGTG 476
Db      421  AGUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 480
Qy      477  CTGCGCTACTGCGGTGGGTAGGAGATCCGGACTGAATCCGATGATTGCGGTACA 533
Db      481  CUGGCAUACUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 537

```

RESULT 5  
ID AAX26111 standard; DNA; 296 BP.  
XX AAX26111;

AC AAX26111;  
XX  
DT 20-MAY-1999 (first entry)

XX Fowlpox virus (FPV S3') LTR sequence.

XX Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;  
XX vaccine; chicken; LTR; long terminal repeat; ss.

OS Fowlpox virus.

XX WO9907852-A1.

XX 18-FEB-1999.

XX 07-AUG-1998; 98WO-AU000628.

XX 08-AUG-1997; 97AU-00008454.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX Hertig C, Coupar BEH, Gould AR, Boyle DB;

XX WPI, 1999-167428/14.

XX Recombinant vaccine against fowlpox virus - is free of contamination from  
XX reticuloendotheliosis virus, used to prevent the virus occurrence in  
XX chickens.

XX Claim 18; Fig 5; 127pp; English.

XX The invention relates to a recombinant fowlpox virus (FPV) whose nucleic  
XX acid does not encode an active reticuloendotheliosis virus (REV), and  
XX whose genome does not contain any REV sequence. The recombinant FPV is  
XX used to produce a vaccine against fowlpox virus. The vaccine is used to  
XX prevent the occurrence of fowlpox virus in chickens. The chickens can be  
XX vaccinated at older than 1 day of age. Alternatively, chickens older than

CC 1 day can be vaccinated with the vaccine subsequent to vaccination with  
CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains  
CC of FPV carry integrated REV sequences. Some of the FPV strains carry a  
CC near full length provirus of REV, and can give rise to infectious REV  
CC when transfected into cell cultures and when chickens are infected. The  
CC present invention provides the means by which a FPV vaccine free from  
CC contamination by REV may be produced. Sequences AAX26110-115 represent  
CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid  
XX molecule can comprise a FPV LTR sequence selected from the above

SQ Sequence 296 BP; 75 A; 58 C; 81 G; 82 T; 0 U; 0 Other;

Query Match

Best Local Similarity 38.7%; Score 206.4; DB 2; Length 296;

Matches 218; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy      1  TGTGGAGGAGGAGTCCGGGGAATGTGGAGGAGAGTCCGGGGGAATAGCGGTGGCTCG 60
Db      1  TGTGGAGGAGGAGTCC-GGGGAATGTGGAGGAGAGTCCGGGGGAATAGCGGTGGCTCG 59
Qy      61  CTAACGCGCATATTAAGCTTCTGTAATCATGCTTTCCTTTCCTTTCCTTTCCTTTCCT 120
Db      60  CTAACGCGCATATTAAGCTTCTGTAATCATGCTTTCCTTTCCTTTCCTTTCCTTTCCT 119
Qy      121  TATATTCGCTGATATCATATTTCTCGGAATCGGCATCAAGACAGGCTCATTAACATAAA 180
Db      120  TATATTCGCTGATATCATATTTCTCGGAATCGGCATCAAGACAGGCTCATTAACATAAA 179
Qy      181  AGGAAATGTTTGTGAAGCAAGCATCAACACACTTGAC 220
Db      180  AGAAATGTTTGTGAAGCAAGCATCAACACACTTGAC 219

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RESULT 6  
ID AAX26115 standard; DNA; 1022 BP.  
XX AAX26115;

XX AAX26115;

XX 20-MAY-1999 (first entry)

XX Fowlpox virus (FPV S) 3' LTR sequence.

XX Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;  
XX vaccine; chicken; LTR; long terminal repeat; ss.

OS Fowlpox virus.

XX WO9907852-A1.

XX 18-FEB-1999.

XX 07-AUG-1998; 98WO-AU000628.

XX 08-AUG-1997; 97AU-00008454.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX Hertig C, Coupar BEH, Gould AR, Boyle DB;

XX WPI, 1999-167428/14.

XX Recombinant vaccine against fowlpox virus - is free of contamination from  
XX reticuloendotheliosis virus, used to prevent the virus occurrence in  
XX chickens.

XX Claim 18; Fig 6; 127pp; English.

XX The invention relates to a recombinant fowlpox virus (FPV) whose nucleic  
XX acid does not encode an active reticuloendotheliosis virus (REV), and  
XX whose genome does not contain any REV sequence. The recombinant FPV is  
XX used to produce a vaccine against fowlpox virus. The vaccine is used to  
XX prevent the occurrence of fowlpox virus in chickens. The chickens can be

CC vaccinated at older than 1 day of age. Alternatively, chickens older than  
CC 1 day can be vaccinated with the vaccine subsequent to vaccination with  
CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains  
CC of FPV carry integrated REV sequences. Some of the FPV strains carry a  
CC near full length provirus of REV, and can give rise to infectious REV  
CC when transfectected into cell cultures and when chickens are infected. The  
CC present invention provides the means by which a FPV vaccine free from  
CC contamination by REV may be produced. Sequences AAX26110-115 represent  
CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid  
CC molecule can comprise a FPV LTR sequence selected from the above

XX Sequence 1022 BP; 315 A; 209 C; 218 G; 280 T; 0 U; 0 Other;

Query Match 38.7%; Score 206.4; DB 2; Length 1022;

Best Local Similarity 99.1%; Pred. No. 2.9e-59; Matches 218; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TGTGGAGGAGCTCCGGGGGAAATGTGGAGGAGCTCCGGGGGAAATAGCGCTGCTCG 60  
DB TGTGGAGGAGCTCCGGGGGAAATGTGGAGGAGCTCCGGGGGAAATAGCGCTGCTCG 467  
QY 61 CTAACTGCCATATTAGCTTCTGTATCATGTGCTTGCCTTACCGCCATTGACTTGA 120  
DB 468 CTAACTGCCATATTAGCTTCTGTATCATGTGCTTGCCTTACCGCCATTGACTTGA 527  
QY 121 TATATTGGCGATATCATTTCTCGAATCGGCATCAAGACAGCTCATTAACCATAAA 180  
DB 528 TATATTGGCGATATCATTTCTCGAATCGGCATCAAGACAGCTCATTAACCATAAA 587  
QY 181 AGAATAATGTTTGTGAAGGAGCATGACACACTTGCAC 220  
DB 588 AGAATAATGTTTGTGAAGGAGCATGACACACTTGCAC 627

RESULT 7  
AAX26112  
ID AAX26112 standard; DNA; 298 BP.

XX AAX26112;

AC 20-MAY-1999 (first entry)

XX Fowlpox virus (FPV M3) LTR sequence.

DE Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;

XX vaccine; chicken; LTR; long terminal repeat; ss.

OS Fowlpox virus.

XX WO9907852-A1.

PN 18-FEB-1999.

XX 07-AUG-1998; 98WO-AU000628.

XX 08-AUG-1997; 97AU-00008454.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX Hertig C, Coupar BEH, Gould AR, Boyle DB;

XX WPI; 1999-167428/14.

XX Recombinant vaccine against fowlpox virus - is free of contamination from

XX PT reticuloendotheliosis virus, used to prevent the virus occurrence in

XX PT chickens.

XX PS Claim 18; Fig 5; 127pp; English.

XX The invention relates to a recombinant fowlpox virus (FPV) whose nucleic

XX acid does not encode an active reticuloendotheliosis virus (REV), and

XX whose genome does not contain any REV sequence. The recombinant FPV is

XX used to produce a vaccine against fowlpox virus. The vaccine is used to

CC prevent the occurrence of fowlpox virus in chickens. The chickens can be  
CC vaccinated at older than 1 day of age. Alternatively, chickens older than  
CC 1 day can be vaccinated with the vaccine subsequent to vaccination with  
CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains  
CC of FPV carry integrated REV sequences. Some of the FPV strains carry a  
CC near full length provirus of REV, and can give rise to infectious REV  
CC when transfectected into cell cultures and when chickens are infected. The  
CC present invention provides the means by which a FPV vaccine free from  
CC contamination by REV may be produced. Sequences AAX26110-115 represent  
CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid  
CC molecule can comprise a FPV LTR sequence selected from the above

XX Sequence 298 BP; 84 A; 59 C; 73 G; 82 T; 0 U; 0 Other;

Query Match 36.2%; Score 193; DB 2; Length 298;

Best Local Similarity 100.0%; Pred. No. 5.5e-55; Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGAAGGAGCTCCGGGGGAAATAGCGCTGCTGCTAACTGCATATTAGCTTGTATC 87  
DB 29 GGAAGGAGCTCCGGGGGAAATAGCGCTGCTGCTAACTGCATATTAGCTTGTATC 88  
QY 88 ATGCTTGCTTGCCTTACCGCCCATTTGACTTGAATATTTGCTGATATCTTCGGA 147  
DB 89 ATGCTTGCTTGCCTTACCGCCCATTTGACTTGAATATTTGCTGATATCTTCGGA 148  
QY 148 ATGCGCATCAAGAGCGCTCATTAACCATTAAGAAATGTTTGTGAAGCAGATC 207  
DB 149 ATGCGCATCAAGAGCGCTCATTAACCATTAAGAAATGTTTGTGAAGCAGATC 208  
QY 208 AGACCACTTGCAC 220  
DB 209 AGACCACTTGCAC 221

RESULT 8  
AAX26114  
ID AAX26114 standard; DNA; 1100 BP.

XX AAX26114;

AC 20-MAY-1999 (first entry)

XX Fowlpox virus (FPV M3) LTR sequence.

DE Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;

XX vaccine; chicken; LTR; long terminal repeat; ss.

OS Fowlpox virus.

XX WO9907852-A1.

PN 18-FEB-1999.

XX 07-AUG-1998; 98WO-AU000628.

XX 08-AUG-1997; 97AU-00008454.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX Hertig C, Coupar BEH, Gould AR, Boyle DB;

XX WPI; 1999-167428/14.

XX Recombinant vaccine against fowlpox virus - is free of contamination from

XX PT reticuloendotheliosis virus, used to prevent the virus occurrence in

XX PT chickens.

XX PS Claim 18; Fig 6; 127pp; English.

XX The invention relates to a recombinant fowlpox virus (FPV) whose nucleic

XX acid does not encode an active reticuloendotheliosis virus (REV), and

XX whose genome does not contain any REV sequence. The recombinant FPV is

CC used to produce a vaccine against fowlpox virus. The vaccine is used to  
CC prevent the occurrence of fowlpox virus in chickens. The vaccine can be  
CC vaccinated at older than 1 day of age. Alternatively, chickens older than  
CC 1 day can be vaccinated with the vaccine subsequent to vaccination with  
CC FPM (FPV mild strain) at 1 day of age. Prior vaccine and field strains  
CC of FPV carry integrated REV sequences. Some of the FPV strains carry a  
CC when full length provirus of REV, and can give rise to infectious REV  
CC present invention provides the means by which a FPV vaccine free from  
CC contamination by REV may be produced. Sequences AAX26110-115 represent  
CC molecule can comprise a FPV LTR sequence selected from the above  
SQ Sequence 1100 BP; 392 A; 177 C; 196 G; 335 T; 0 U; 0 Other;

Query Match 36.2%; Score 193; DB 2; Length 1100;  
Best Local Similarity 100.0%; Pred. No. 1.1e-54;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 GAGAGGAGCTCCGGGGGAAATAGCGTGGCTGCTAAGCAATTAAGTTCTGTATC 87  
DB 908 GAGAGGAGCTCCGGGGGAAATAGCGTGGCTGCTAAGCAATTAAGTTCTGTATC 87  
QY 88 ATGCTTGCTGCTTACCGCGCATTTGATTAATTTGCGATATCATTTTCGGA 147  
DB 968 ATGCTTGCTGCTTACCGCGCATTTGATTAATTTGCGATATCATTTTCGGA 1027  
QY 148 ATCGGATCAAGAGAGGCTCATTAACCATTAAGAAATGTTGTTGAAGCAAGCATC 207  
DB 1028 ATCGGATCAAGAGAGGCTCATTAACCATTAAGAAATGTTGTTGAAGCAAGCATC 1087  
QY 208 AGACCACTTGCAAC 220  
DB 1088 AGACCACTTGCAAC 1100

RESULT 9  
ADE87477  
ID ADE87477 standard; DNA; 266145 BP.

AC ADE87477;  
DT 29-JAN-2004 (first entry)  
DB Fowlpox virus genome DNA.  
XX  
KM fowlpox virus; FPV; virulence; tuberculostatic; protozoacide; antipyrretic;  
KM cytotaxic; hepatotropic; antibacterial; vaccine; malaria; tuberculostatic;  
KM East Coast fever; avipox virus; influenza; hepatitis;  
KM human papilloma virus; tumour; leishmaniasis; listeriosis; theileria;  
KM gene; db.  
XX

OS Fowlpox virus.  
PN WO2003047617-A2.  
PD 12-JUN-2003.  
PF 02-DEC-2002; 2002WO-GB005411.  
XX  
XX 30-NOV-2001; 2001GB-00028733.  
PR 30-NOV-2001; 2001US-0334649P.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX  
PI Laidlaw S, Skinner M, Hill A, Gilbert S, Anderson R;  
XX WPI; 2003-513700/48.  
XX

PT Treating and/or preventing e.g. malaria or tuberculostatic, or eliciting an  
PT immune response, comprises administering a priming composition and a  
PT boosting composition containing a non-replicating viral vector in either  
PT order.

XX  
XX Claim 30; SEQ ID NO 1; 302pp; English.

CC The invention relates to a fowlpox virus (FPV) genome which has  
CC modifications in one or more wild-type FPV genes. The invention further  
CC relates to a novel method for treating and/or preventing a disease in a  
CC subject comprising administering two compositions, each containing a non-  
CC poxvirus vector derived from a fowlpox virus. The novel compositions comprise a  
CC the following activities: virulence, tuberculostatic, protozoacide,  
CC antipyrretic, cytotaxic, hepatotropic, and antibacterial. The non-  
CC replicating viral vector is useful in a vaccine for an animal,  
CC particularly a mammal such as a primate, specifically human. The priming  
CC or boosting composition, or the kit is useful for manufacturing a  
CC medicament for treating and/or preventing a disease which is, or results  
CC from, a chronic infection such as malaria, tuberculostatic or East Coast  
CC fever, or for eliciting a T-cell immune response in a subject. Non-  
CC cultured CEF cells are useful for growing an avipox virus, such as  
CC fowlpox virus. The method or the vaccine may further be used to treat or  
CC prevent influenza, hepatitis, human papilloma virus and other viral  
CC infections, malignancies such as tumours, leishmaniasis, listeriosis, and  
CC virus genome of the invention.

Sequence 266145 BP; 92375 A; 41026 C; 40846 G; 91897 T; 0 U; 1 Other;  
Query Match 36.2%; Score 193; DB 9; Length 266145;  
Best Local Similarity 100.0%; Pred. No. 2e-53;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GAGAGGAGCTCCGGGGGAAATAGCGTGGCTGCTAAGCAATTAAGTTCTGTATC 87  
DB 221741 GAGAGGAGCTCCGGGGGAAATAGCGTGGCTGCTAAGCAATTAAGTTCTGTATC 221800  
QY 88 ATGCTTGCTGCTTACCGCGCATTTGATTAATTTGCGATATCATTTTCGGA 147  
DB 221801 ATGCTTGCTGCTTACCGCGCATTTGATTAATTTGCGATATCATTTTCGGA 221860  
QY 148 ATCGGATCAAGAGAGGCTCATTAACCATTAAGAAATGTTGTTGAAGCAAGCATC 207  
DB 221861 ATCGGATCAAGAGAGGCTCATTAACCATTAAGAAATGTTGTTGAAGCAAGCATC 221920  
QY 208 AGACCACTTGCAAC 220  
DB 221921 AGACCACTTGCAAC 221933

RESULT 10  
AAV63779  
ID AAV63779 standard; DNA; 578 BP.

AC AAV63779;  
DT 17-MAR-1999 (first entry)  
DB Sequence derived from the 5' end of REV-A.  
XX  
XX Reticuloendotheliosis virus type A; REV-A; 5' end genomic RNA;  
KM type C retrovirus; internal ribosome entry site; IRBS; encapsidation;  
KM retroviral vector; gene therapy; ss.  
XX

OS Reticuloendotheliosis virus.  
PN FR2762615-A1.  
PD 30-OCT-1998.  
XX

PF 28-APR-1997; 97FR-00005203.  
XX  
XX 28-APR-1997; 97FR-00005203.  
PR 28-APR-1997; 97FR-00005203.  
XX

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
XX



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PI Lopez Lastera M., Gabus Darlax C., Darlax JL;
XX WPI: 1999-037487/04.
DR
XX Expression vectors containing IRES and/or encapsidation enhancer -
PT derived from type C retrovirus other than FMLV and MoMLV.
XX
PS Claim 6; Page 32; 43pp; French.
XX
CC The present sequence is derived from the 5' end of the genomic RNA of
CC Reticuloendotheliosis virus type A (REV-A). The specification also
CC describes nucleotide sequence derived from all or part of the 5' end of
CC the genomic RNA of a type C retrovirus other than Fowl and murine leukaemia
CC virus (FMLV) and Moloney murine leukaemia virus (MoMLV). The 5' derived
CC sequences are used as an internal ribosome entry site (IRES) in a vector
CC for permitting or enhancing the encapsidation of a retroviral vector. The
CC vectors can be used for gene therapy, production of recombinant
CC polypeptides or production of transgenic animals
XX
SQ Sequence 578 BP; 94 A; 139 C; 172 G; 0 T; 173 U; 0 Other;
Query Match 29.1%; Score 155; DB 2; Length 578;
Best Local Similarity 67.4%; Pred. No. 7e-42;
Matches 118; Conservative 51; Mismatches 5; Indels 1; Gaps 1
QY 360 GGGGTGCGCGCTCTACACATTGTTGTAGTCGCGGCCGACATTCGAATCTGTATAAAG 419
Dd 1 GGGGCGCGCGCUCUACAUUUUGUAGACGCGGCCCGACAUUCGAUUCGUAAUAAAAG 60
QY 420 -CTTTCCTCATATNCCCTCAGATTGGCAGTGAGAGAATTTGTTCGTGTTGCT 478
Dd 61 UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 120
QY 479 GGCTACTGCGGTGGGTAGGATCCGCACTGATTCGTATTTGGTAGAACACA 533
Dd 121 GGCCTACUGGGGUGGGUGAGGGUCCGCAUCGAUUCGUAGUAUUUGCAUACA 175
RESULT 11
AAQ76041
ID ID AAQ76041 standard; DNA; 3878 BP.
XX
XX AAQ76041;
XX 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Retrovirus vector pPolis-R1.
XX
XX Retrovirus; vector; pPolis-R1; spleen necrosis virus; SNV; gene transfer;
FM gene therapy; ss.
XX
OS Spleen necrosis virus.
XX
W09429437-Al.
PD 22-DEC-1994.
PF 07-JUN-1994; 94MO-US006415.
PR 07-JUN-1993; 93US-00073345.
PA (UYNE-) UNIV NEW JERSEY.
XX
XX Dornburg RC;
XX WPI: 1995-036467/05.
XX Recombinant retrovirus vector, contg. non-retroviral gene, - has ability
PT to produce progeny virus, in helper cell which can infect host cell and
XT form provirus.
XS Example; Page 17; 28pp; English.
```

XX	The universal retroviral vector pPol15-R1 (given in AA076041) was
CC	obtained by replacing the SV40 promoter and hpt gene of pPol11-R1
CC	(AA076038) with the multiple cloning site of Bluescript II KS. The
CC	vectors allow cell-type specific gene expression and eliminate risks of
CC	downstream activation of cellular proto-oncogenes. (Updated on 25-MAR-
CC	2003 to correct PN field.)
XX	
SQ	Sequence 3878 BP; 922 A; 948 C; 988 G; 1020 T; 0 U; 0 Other;
	Query Match            27.2%; Score 145; DB 2; Length 3878;
	Best Local Similarity    90.4%; Pred.No. 4.9e-38;
	Matches 189; Conservative 0; Mismatches 15; Indels 5; Gaps 3;
OY	330 GCCTATATAAGCCACGCGCATCTTGTGTCGGGGTGCCGCCCTCACACA---TTGTTGTCG 386
DB	654 GTCTATTATTAACAGAGCTCATCTTGTGTCGGGGTGCCGCCCTGCACATTGTTGTTGTG 713
OY	387 ACGTGCGGCCCCAGATTCGAATCCTGTAATTAANA-GCTTTTTTCTATATCCTCAGATTGG 445
DB	714 ACGTGGCGGCCCAATTCGAATCTGTAATTAANAACCTTTTTTTCTGAATCCTCAGATTGG 773
OY	446 CAGTGAGAGAGATTTTGTTCGTGTGCTGTGCTGCGCTGACTGAGGTGGG-GTAGGGATCCG 504
DB	774 CAGTGAGAGAGATTTTGTTCGTGTGCTGTGCTGCGCTGACTGAGGTGGGCGCAGGGATCCG 833
OY	505 GACTGAATCCGTAGTATTTCGGTACACA 533
DB	834 GACTGAATCCGTAGTACTTCGGTACACA 862
RESULT 12	
AA076038	
ID	AA076038 standard; DNA; 5528 BP.
XX	
AC	AA076038;
XX	
DT	25-MAR-2003 (revised)
DT	20-JUN-1995 (first entry)
XX	
DE	Retrovirus vector pPol11-R1.
XX	
KM	Retrovirus; vector: pPol11-R1; spleen necrosis virus; SNV;
KM	Cyomegalovirus; CMV; intermediate-early promoter; IE promoter;
KM	long terminal repeat; LTR; encapsidation; gene transfer; gene therapy;
ss.	
XX	
OS	Spleen necrosis virus.
XX	
FN	W09429437-A1.
PD	22-DEC-1994.
XX	
PF	07-JUN-1994; 94WO-US006415.
XX	
FR	07-JUN-1993; 93US-00073345.
PA	(UYNE-) UNIV NEW JERSEY.
XX	
P1	Dornburg RC;
XX	
DR	WPI; 1995-036467/05.
PT	
PT	Recombinant retrovirus vector, contg. non-retroviral gene, - has ability
PT	to produce progeny virus, in helper cell which can infect host cell and
PT	form provirus.
XX	
PS	Example; Page 13-14; 28pp; English.
CC	New recombinant-free, highly efficient retroviral vectors pPol11-R1
CC	(given in AA076038), pPol11-R2 (AA076039) and pPol11-R3 (AA076040) were
CC	obtained by replacing the U3 region of the left LTR of spleen necrosis
CC	virus with the IE promoter/enhancer of CMV, and extension of the

Sequence 5519 BP; 1264 A; 1420 C; 1456 G; 1379 T; 0 U; 0 Other;

Query Match	23.9%;	Score	127.6;	DB	2;	Length	5519;
Best Local Similarity	92.3%;	Pred. No.	5e-32;				



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```

CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312837)..(312837)
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
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NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1115881)..(1115881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g

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Query Match 6.08; Score 32; DB 4; Length 9347;

NAME/KEY:	intron
LOCATION:	584-325

LOCATION: 584...325'

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FEATURE:
NAME/KEY: exon
LOCATION: 3258..3449
FEATURE:
NAME/KEY: intron
LOCATION: 3450..3938
FEATURE:
NAME/KEY: exon
LOCATION: 3939..4122
FEATURE:
NAME/KEY: intron
LOCATION: 4123..5042
FEATURE:
NAME/KEY: exon
LOCATION: 5043..5270
FEATURE:
NAME/KEY: intron
LOCATION: 5271..5830
FEATURE:
NAME/KEY: exon
LOCATION: 5831..5944
FEATURE:
NAME/KEY: intron
LOCATION: 5945..6632
FEATURE:
NAME/KEY: exon
LOCATION: 6633..6758
FEATURE:
NAME/KEY: intron
LOCATION: 6759..6966
FEATURE:
NAME/KEY: exon
LOCATION: 6967..7252
FEATURE:
NAME/KEY: intron
LOCATION: 7253..7870
FEATURE:
NAME/KEY: exon
LOCATION: 7871..8102
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 8103..8537
FEATURE:
NAME/KEY: misc RNA
LOCATION: 8538..8878
FEATURE:
NAME/KEY: CDS
LOCATION: join(470..583, 3258..3449, 3939..4122, 5043..5270,
5831..5944, 6633..6758, 6967..7252, 7871..8102)
US-08-206-176-3

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Query Match          5.9%; Score 31.4; DB 1; Length 8878;
Best Local Similarity 57.7%; Pred. No. 3.5;
Matches 56; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 84 AATATGCTTGGCTTACCTTACCGCCATGTCATGATATATTCGCTGATATCATTTCT 143
DB 1109 AAAAAGCAATATTTCAATTTCTATCATATACCTGATGATATTTCTTTAGCTTTAGT 1050
QY 144 CGGAATCGGATCAGAGCAGGCTCAATAAACCTAA 180
DB 1049 TATATTTTATATATATATGATATCTCAGTAAACAATATA 1013

```

RESULT 5  
US-08-943-731-1

```

; Sequence 1, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILIA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, IARISA

```

```

APPLICANT: LARSON, ANDREA W.
APPLICANT: PACK, MICHAEL
APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORRKO, JARMO
APPLICANT: ALA-KORRKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
ADDRESS: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18609 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-943-731-1

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Query Match          5.9%; Score 31.4; DB 3; Length 18609;
Best Local Similarity 53.7%; Pred. No. 5.7;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 398 AGATTCGAATCTGTATATAAGCTTTTCTTATATCTCTAGATTGGCAGTGAAGAG 457
DB 5386 AGGTAAAGGCTGTCTGAACATCATGTCCTCCACATCCCAAGATCCACATGAATGA 5345
QY 458 ATTTTGTCTGAGGTTGGCTGCTACTGAGTGGGGGTAGGGATCCGACTGAATCCGTA 517
DB 5346 ATTTTCATCATATATTTCTTCTGATCTACAGAGGTGAGCTTGAGCCCTGGTGAAATGGA 5405
QY 518 G 518
DB 5406 G 5406

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RESULT 6  
US-09-453-702B-111/C

```

; Sequence 111, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; BURLAND, Valerie

```



```

1 LENGTH: 832
2 TYPE: DNA
3 ORGANISM: Homo sapiens
4 FEATURE:
5 NAME/KEY: CDS
6 LOCATION: 235..399
7 US-09-621-976-2813

Query Match 5.7%; Score 30.4; DB 4; Length 832;
Best Local Similarity 10.6%; Pred. No. 1.8;
Matches 28; Conservative 120; Mismatches 116; Indels 0; Gaps 0;

Oy 64 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 123
Db 110 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 169
Oy 124 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 183
Db 170 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 229
Oy 184 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 243
Db 230 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 289
Oy 244 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 303
Db 290 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 349
Oy 304 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 367
Db 350 AATGCGATATATGCTTCTGTAATATGCTTCTGCGCTTACGCCATTCGATTTGATAT 419

RESULT 8
US-10-204-708-45/C
Sequence 45, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIORITY APPLICATION NUMBER: PCT/EP01/03971
PRIORITY FILING DATE: 2001-04-06
PRIORITY APPLICATION NUMBER: DE 10019058.8
PRIORITY FILING DATE: 2000-04-06
PRIORITY APPLICATION NUMBER: DE 10019173.8
PRIORITY FILING DATE: 2000-04-07
PRIORITY APPLICATION NUMBER: DE 10032529.7
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: DE 10043826.1
PRIORITY FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 45
LENGTH: 19233
TYPE: DNA
FEATURE:
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
NAME/KEY: unsure
LOCATION: (76, 178..179, 273, 586, 648, 651, 920, 1014, 1173, 1197, 1228)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure

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LOCATION: (2168, 2254, 2257, 2280, 2291, 2723, 3018, 3080, 4205, 4209)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (4216, 4225, 4239, 4246, 4254, 4265, 4270, 4274, 4288, 4294..4295)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (4298, 4363, 4610, 4627, 4675, 4693, 4698, 4738, 4777, 4781)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (4787, 4825, 4829, 4838, 4855, 5462, 5494, 5496, 5500, 5674)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (5690, 5697, 5705, 5715, 5890, 5910, 5913, 6027, 6080, 6109)
OTHER INFORMATION: n is a or g or c or t
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NAME/KEY: unsure
LOCATION: (6244, 6288, 6776, 6873, 6891, 6980, 7028, 7656, 7876, 8030)
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FEATURE:
NAME/KEY: unsure
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OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (10005, 10075, 10150, 10159, 10165, 10356, 11123, 11166, 11360)
OTHER INFORMATION: n is a or g or c or t
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NAME/KEY: unsure
LOCATION: (13846, 14168, 16566, 17006, 17217, 17650, 17653, 17656, 17898)
OTHER INFORMATION: n is a or g or c or t
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OTHER INFORMATION: n is a or g or c or t
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NAME/KEY: unsure
LOCATION: (19200)
OTHER INFORMATION: n is a or g or c or t
US-10-204-708-45

Query Match      5.7%; Score 30.4; DB 4; Length 19233;
Best Local Similarity 56.7%; Pred. No. 13;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 169 ATAAACCATTAAGAAATGTTGTTGAGCAAGCATGACCACTTGACATCCAAAT 228
Db 17016 ATAAATAATTAACCAATATTAACCTACGCCCTATATCTTAACATTTAAAAACCAA 16957
QY 229 CAGCAAAACAGCAGATGCACTATATCTGAGCC 265
Db 16956 ATAAAAAATCAGCAATCAAAAAATTAACCATCC 16920

RESULT 9
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
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NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
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LOCATION: (255001) ..(270000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (270001) ..(285000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (285001) ..(300000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (300001) ..(315000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (315001) ..(330000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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LOCATION: (330001)..(345000)  
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NAME/KEY: misc feature  
LOCATION: (345001)..(360000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (360001)..(375000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (375001)..(390000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (390001)..(405000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (405001)..(420000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (420001)..(435000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (435001)..(450000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (450001)..(465000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (465001)..(480000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (480001)..(495000)  
OTHER INFORMATION: n=a or c or g or t  
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LOCATION: (495001)..(510000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
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OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (525001)..(540000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (540001)..(555000)  
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NAME/KEY: misc feature  
LOCATION: (570001)..(585000)  
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NAME/KEY: misc feature  
LOCATION: (600001)..(615000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (615001)..(630000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (630001)..(645000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (645001)..(660000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (660001)..(675000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (675001)..(690000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (690001)..(705000)

OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (705001)..(720000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (720001)..(735000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (735001)..(750000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (750001)..(765000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (765001)..(780000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (780001)..(795000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (795001)..(810000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (810001)..(825000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (825001)..(840000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (840001)..(855000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (855001)..(870000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (870001)..(885000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (885001)..(900000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (900001)..(915000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature

Query Match 5.7%; Score 30.4; DB 4; Length 1230025;  
Best Local Similarity 54.5%; Pred. No. 1.5e+02;  
Matches 61; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 17 GGGGGAATGGAGGAGGAGCTCGGGGGGAATGAGCGCTGCTGCTAAGTGCATATTTAG 76  
Db 638954 GGAAGTATATCTCATGATTCATGAGAGGATGGCTTACCTTATGATACATATTAAG 639013  
Qy 77 CTTCGTAATCATGCTGCTGCTTGGCTTACCGCCATTGTAATATTTTC 128  
Db 639014 CTTCATCTCTCTTTTTCCTATGATGAGCATTTAGACTATTTTTC 639065

RESULT 10  
US-09-221-298-77/c  
Sequence 77, Application US/09221298  
Patent No. 6284241  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS  
FILE REFERENCE: 210121.471  
CURRENT FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 77  
LENGTH: 458

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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (196)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (335)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (409)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (410)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (417)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (442)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (447)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (450)
; OTHER INFORMATION: Where n is a, c, g or t
; US-09-221-298-77

Query Match
Best Local Similarity 5.7%; Score 30.2; DB 3; Length 458;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 376 ACATTGTTGACGTCGCGCCGACGATTCGATGATTAAGCTTTTCTCTATATC 435
DB 287 ACATATTTGGAGATTAAGTATAGTATGATGTTTCCAAAGCTTTTCTCTTATTC 228
QY 436 CTCAGATTGCGACGTGAGAGAGATTTTGTGTCGTGTGCTTGCTTACTGAGT 491
DB 227 CTCATATGAGAAATGAAGAGCATTACCATTTTGGGGTAGAGCTGTCTGTTG 172

RESULT 11
US-09-401-064-77/c
; Sequence 77, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (1)...(458)
; OTHER INFORMATION: n = A,T,C or G
; US-09-401-064-77

Query Match
Best Local Similarity 5.7%; Score 30.2; DB 4; Length 458;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 376 ACATTGTTGACGTCGCGCCGACGATTCGATGATTAAGCTTTTCTCTATATC 435
DB 287 ACATATTTGGAGATTAAGTATAGTATGATGTTTCCAAAGCTTTTCTCTTATTC 228
QY 436 CTCAGATTGCGACGTGAGAGAGATTTTGTGTCGTGTGCTTGCTTACTGAGT 491
DB 227 CTCATATGAGAAATGAAGAGCATTACCATTTTGGGGTAGAGCTGTCTGTTG 172

RESULT 12
US-08-961-527-145/c
; Sequence 145, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-145

Query Match
Best Local Similarity 5.7%; Score 30.2; DB 4; Length 10711;
Matches 112; Conservative 0; Mismatches 118; Indels 1; Gaps 1;

QY 210 ACCACTTGACCATCATCAGCAAGCAAGAGATGCAACTATCATCTAGCGCAATG 269
DB 5925 ACGAATTTATCAAAATAGTGTCTTGATCACCAAGCTTCACACTCAATGTAGGTAC 5866
QY 270 GTTGTAAAGGCGAGATCTATCTCCCAATGAGGAAATGTCATGCAACATCTGTAAGC 329
DB 5865 ATTGAGAGCTCGCTCGATTGTAAAGAGCGTAAAGTTTGGAGTAATCTGTATC 5806
QY 330 GGCTATATAAGCGAGGTGATCTTGTGCTGGGGTCCGCTCTACACATTTGTGTAGC 389
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Db 5805 GTCACTGTGACATTTGTCAGACGTGATTTGTGGCGCTTAACATAGTTGAG-CG 5747  
Qy 390 TGGGGCCCAATTCGATCTGTATTAAGCTTTTCTTCTATTCCTCG 440  
Db 5746 CGAGAGACTTATGTGATAGTACTCTTTTTCACCGATTTACAG 5696

## RESULT 13

US-08-816-346-5  
; Sequence 5, Application US/08816346  
; Patent No. 6127525  
; GENERAL INFORMATION:  
; APPLICANT: Crystal, Ronald G.  
; APPLICANT: Falck-Pedersen, Erik  
; APPLICANT: Gail, Jason  
; APPLICANT: Kovesdi, Imre  
; APPLICANT: Wickham, Thomas J.  
; TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND  
; TITLE OF INVENTION: METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
; STREET: TWO PRUDENTIAL PLAZA - 4900  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60601-6780  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,346  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; REFERENCE/DOCKET NUMBER: 67167  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/616-5600  
; TELEFAX: 312/616-5700  
; TELEX: 25-3533  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 603 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-816-346-5

Query Match 5.6%; Score 30; DB 3; Length 603;  
Best Local Similarity 55.9%; Pred. No. 2;  
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 97 TGCCTTAGCCGCATTTGATATATTTGCTGATATCATTTTCGGAATGGCATC 156  
Db 410 TGCTCTTCCAAAGTTGACTGCAATCTTCTCAATACCTCTTTGAACGACCGGC 469  
Qy 157 AAGAGCAGCTCATTAACCATTAAGAAATGTTTGTGAAG 198  
Db 470 AAGGCATGCTACTTAACCAAAAGTGTGTTTGTACAGTGAAG 511

## RESULT 14

US-09-335-411-5  
; Sequence 5, Application US/09335411  
; Patent No. 6153435  
; GENERAL INFORMATION:  
; APPLICANT: Crystal, Ronald G.  
; APPLICANT: Falck-Pedersen, Erik  
; APPLICANT: Gail, Jason

APPLICANT: Kovesdi, Imre  
APPLICANT: Wickham, Thomas J.  
TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND  
TITLE OF INVENTION: METHODS OF USING SAME  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
STREET: TWO PRUDENTIAL PLAZA - 4900  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,411  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,346  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 67167  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/616-5600  
TELEFAX: 312/616-5700  
TELEX: 25-3533  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-335-411-5

Query Match 5.6%; Score 30; DB 3; Length 603;  
Best Local Similarity 55.9%; Pred. No. 2;  
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 97 TGCCTTAGCCGCATTTGATATATTTGCTGATATCATTTTCGGAATGGCATC 156  
Db 410 TGCTCTTCCAAAGTTGACTGCAATCTTCTCAATACCTCTTTGAACGACCGGC 469  
Qy 157 AAGAGCAGCTCATTAACCATTAAGAAATGTTTGTGAAG 198  
Db 470 AAGGCATGCTACTTAACCAAAAGTGTGTTTGTACAGTGAAG 511

RESULT 15  
US-08-816-346-1  
; Sequence 1, Application US/08816346  
; Patent No. 6127525  
; GENERAL INFORMATION:  
; APPLICANT: Crystal, Ronald G.  
; APPLICANT: Falck-Pedersen, Erik  
; APPLICANT: Gail, Jason  
; APPLICANT: Kovesdi, Imre  
; APPLICANT: Wickham, Thomas J.  
; TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND  
; TITLE OF INVENTION: METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
; STREET: TWO PRUDENTIAL PLAZA - 4900  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60601-6780  
; COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/816,346
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ REFERENCE/DOCKET NUMBER: 67167
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/616-5600
/ TELEFAX: 312/616-5700
/ TELEX: 25-3533
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2907 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-816-346-1

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Query Match      5 6%; Score 30; DB 3; Length 2907;
Best Local Similarity 55.9%; Pred. No. 5.5;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY      97 TGCCTTAGCCGCGCATTTGACTTGATATATATTTGCTGATATATCTCGAATGCGCATC 156
      |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      803 TGCCTCTTCCAAAGGTGACTTGCAATCTCTCAAAATCTACTACTCTTTGAACGACCGGC 862

QY      157 AAGACAGGCTATATAACCATTAAGAAAGAAATGTTGTGAAG 198
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DB      863 AAGCAATGCTACTAAACCAAAAGTGTTTGTACAGTGAAG 904

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Search completed: May 25, 2004, 02:59:18  
 Job time : 92 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 01:32:27, Search time 339 Seconds

(without alignments)  
7145.545 Million cell updates/sec

Title: US-10-623-891-2

Perfect score: 533

Sequence: 1 tggggagggaggtccggggg.....cgtgatttcgtacacaa 533

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2953838 seqs, 2272363821 residues

Total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PC7\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PC7US\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10C\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	6.6	328	13	US-10-142-426-34
2	35	6.6	328	15	US-10-123-155-34
3	35	6.6	328	15	US-10-146-731-34
4	35	6.6	328	15	US-10-140-472-34
5	35	6.6	328	15	US-10-141-761-34
6	35	6.6	328	15	US-10-142-885-34
7	35	6.6	328	15	US-10-158-790-34
8	35	6.6	328	15	US-10-137-871-34
9	35	6.6	328	16	US-10-140-823-34
10	35	6.6	328	16	US-10-141-756-34
11	35	6.6	328	16	US-10-141-759-34
12	35	6.6	328	16	US-10-140-805-34
13	35	6.6	328	16	US-10-140-864-34
14	35	6.4	616	13	US-10-142-426-206

15	34	6.4	616	15	US-10-123-155-206	Sequence 206, App
16	34	6.4	616	15	US-10-146-731-206	Sequence 206, App
17	34	6.4	616	15	US-10-140-472-206	Sequence 206, App
18	34	6.4	616	15	US-10-141-761-206	Sequence 206, App
19	34	6.4	616	15	US-10-142-885-206	Sequence 206, App
20	34	6.4	616	15	US-10-158-790-206	Sequence 206, App
21	34	6.4	616	16	US-10-137-871-206	Sequence 206, App
22	34	6.4	616	16	US-10-140-923-206	Sequence 206, App
23	34	6.4	616	16	US-10-141-756-206	Sequence 206, App
24	34	6.4	616	16	US-10-141-759-206	Sequence 206, App
25	34	6.4	616	16	US-10-140-805-206	Sequence 206, App
26	34	6.4	616	16	US-10-140-864-206	Sequence 206, App
27	33.4	6.3	6617	13	US-10-449-462-1	Sequence 1, Appl1
28	33.4	6.3	6617	15	US-10-210-296-1	Sequence 1, Appl1
29	32.8	6.2	802	15	US-10-184-644-312	Sequence 312, App
30	32.8	6.2	802	15	US-10-184-644-312	Sequence 312, App
31	32.8	6.2	25519	13	US-10-087-192-1207	Sequence 1207, App
32	32.6	6.1	650	13	US-10-027-632-1039	Sequence 1039, App
33	32.6	6.1	650	13	US-10-027-632-1040	Sequence 1040, App
34	32.6	6.1	650	13	US-10-027-632-1041	Sequence 1041, App
35	32.6	6.1	650	16	US-10-027-632-1039	Sequence 1039, App
36	32.6	6.1	650	16	US-10-027-632-1040	Sequence 1040, App
37	32.6	6.1	650	16	US-10-027-632-1041	Sequence 1041, App
38	32.6	6.1	96595	12	US-10-052-482-232	Sequence 232, App
39	32.2	6.0	3388	13	US-10-416-592-8	Sequence 8, Appl1
40	32.2	6.0	3410	15	US-10-120-988-225	Sequence 225, App
41	32.2	6.0	20346	5	US-10-123-9658-1	Sequence 1, Appl1
42	32	6.0	19319	13	US-10-424-599-27873	Sequence 27873, A
43	32	6.0	9347	13	US-10-204-708-36	Sequence 36, Appl1
44	32	6.0	397658	9	US-09-813-320-3	Sequence 3, Appl1
45	31.4	5.9	601	13	US-10-027-632-89624	Sequence 89624, A

#### ALIGNMENTS

RESULT 1  
US-10-142-426-34/c  
; Sequence 34, Application US/10142426  
; Publication NO. US20040048333A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P333081C224  
; CURRENT APPLICATION NUMBER: US/10/142, 426  
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 34  
; LENGTH: 328  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
; US-10-142-426-34  
Query Match 6.6%; Score 35; DB 13; Length 328;  
Best Local Similarity 6.9%; Pred. No. 0.67;

[illegible]

```

RESULT 2
US-10-123-155-34/C
; Sequence 34, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivartoff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P33081C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; PRIOR FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-123-155-34

```

Query Match	6.6%;	Score 35;	DB 15;	Length 328;
Best Local Similarity	6.9%;	Pred. No. 0.67;		
Matches	21;	Conservative	98;	Mismatches 184.
				Indels 0.
				Cons 0

QY	10	TTTGCCGCATTTGTCATATATTTGGTCGATATCATCTTTCTCGAATCGCATCAAGA	160
Db	322	BRY..M.TYNN..GHMC..S..N..NAI..GNN..B..Y..NHSSX...S..N..S..Y..SDK..	263
QY	161	GCAGGCTCATTAACCATTAAGAAATGTTTGTGAAGGCAAGCATCAGCCACTTGAC	220
Db	262	KTA..RB..NMK..WSTY..RG..AKSCHEA..SSA..R...N..C...RTINMEA..YA..AH	203

Qy	221	CATCCAAATCAGAAACAAACACGAGATCCAAATATCTACTAGCCCAATGTTGTTAAAGG	280
Db	202	YN.KTN...NSHSBM...SBBB.CN.SMTT.ABNAR.DNND...B.CS.T.CN..D.S	143
Qy	281	CAGATGCTATCTCCATCAGTAGGGGAAATGCAATGCAATCTCTGAAGCGGCTATATTAAG	340
Db	142	C.SH.SC.D.Y...YDSRAK.CCS.NB.D.NH.Y.SBDYCANRRACGBMYCCAN.Y..A	83
Qy	341	CCAGGTGATCTCTTGGCTCGGGTCGCGCTCTTACACATTTGTTGACGTCGGGCCGAGA	400
Db	82	...H..KDSA..NB.S.YMCBSG.NMTSNB.CM.S.B.B.SC.BB.MRTMWC.D.M.SN.	23
Qy	401	TTC	403
Db	22	TS	20

```

US-10-146-731-34/C
; Sequence 34, Application US/10146731
; Publication No. US20030129692A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C323
; CURRENT APPLICATION NUMBER: US/10/146,731
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-146-731-34

```

Query Match	Score 35;	DB 15;	Length 328;
Best Total Similarity	6.6%		

best local similarity 6.9%; Pred. NO. 0.67;  
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

Dy 101 TTAGCCGCATGTTACTGTATATTTCGGTATCATTTCTCGGAATCGGCATCAAGA 160  
:: :: : |::| : : : : : : : :  
Db 322 BTR..M.TYNN.GHMC...S.N..NAY.GYNN...B.Y..NHSKS....S..N.S...Y.SDX, 263

Dy 161 GCAGGCTCATAAACCATTAAGAAATGTTTGTTGAAGCAACATCAGACCCTTGCAC 220  
::|| :: : : : : :  
Db 262 KTA.RB.MNK..WSTA.RG..AKSCHRA..SSA..R...N.C...ETHNMFA.YA.AH 203

Dy 221 CATCCATCACAACAAACAGATGACACTCATACTGAGCCAACTGGTTGTAAAGG 280  
Db 202 YN.KYN..NSHSHBM..SBBB.CN.SMTT.ABNAR...DNRD...B.CS.T.CN.D.S 143

CY 281 CAGATGCTATCCTCCATGAGGGAAATGTCAACCATCCTGTAAACCGGTATATAAG 340  
| : : | : : : : : : : : : : : : : : : : : :  
Db 142 C.SH.SC.D.Y....YDSRAK.CCS.NB.D.MH.Y.SBDYCANKRACSMBMYCAN.Y..A 83



QY 341 CAGAGTCATCTCTGCTCGGCGTCCGCTTACACATTTGTGTGACGTGCGGCCGAGA 400  
DB 82 ...H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SC.BB.MRTWMC.D.M.SN. 23  
QY 401 TTC 403  
DB 22 .TS 20

## RESULT 4

US-10-140-472-34/c  
; Sequence 34, Application US/10140472  
; Publication No. US20030138888A1  
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Collin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C168  
CURRENT APPLICATION NUMBER: US/10/140,472  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 34  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-472-34

Query Match 6.6%; Score 35; DB 15; Length 328;  
Best Local Similarity 6.9%; Pred. No. 0.67;  
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCGCCATCTGCTGATATATTTGCGTGAATATTCATTTCCGAAATCGCATCAGA 160  
DB 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK. 263  
QY 161 GCAGGCTCATTAACCAATAAAGAAATGTTGTGAAGGAGCATCAGACCACTTGAC 220  
DB 262 KVA.RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTNMPA.YA.AH 203  
QY 221 CATCCATATCAGAAACAGAGATGAATCATATCATCTGAGCCATGTTGAAGGG 280  
DB 202 YN.KYN...NSSHBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143  
QY 281 CAGATGCTATCTCTGCTGAGGAAATGTCATCAATCTGAGCGGCTATATAG 340  
DB 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKAESBMYCCAN.Y..A 83  
QY 341 CAGAGTCATCTCTGCTCGGCGTCCGCTTACACATTTGTGTGACGTGCGGCCGAGA 400  
DB 82 ...H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SC.BB.MRTWMC.D.M.SN. 23  
QY 401 TTC 403  
DB 22 .TS 20

RESULT 5  
US-10-141-761-34/c  
; Sequence 34, Application US/10141761  
; Publication No. US20030148432A1  
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Collin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C198  
CURRENT APPLICATION NUMBER: US/10/141,761  
CURRENT FILING DATE: 2002-05-08  
Prior Application removed - See File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 34  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-141-761-34

Query Match 6.6%; Score 35; DB 15; Length 328;  
Best Local Similarity 6.9%; Pred. No. 0.67;  
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCGCCATCTGCTGATATATTTGCGTGAATATTCATTTCCGAAATCGCATCAGA 160  
DB 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK. 263  
QY 161 GCAGGCTCATTAACCAATAAAGAAATGTTGTGAAGGAGCATCAGACCACTTGAC 220  
DB 262 KVA.RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTNMPA.YA.AH 203  
QY 221 CATCCATATCAGAAACAGAGATGAATCATATCATCTGAGCCATGTTGAAGGG 280  
DB 202 YN.KYN...NSSHBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143  
QY 281 CAGATGCTATCTCTGCTGAGGAAATGTCATCAATCTGAGCGGCTATATAG 340  
DB 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKAESBMYCCAN.Y..A 83  
QY 341 CAGAGTCATCTCTGCTCGGCGTCCGCTTACACATTTGTGTGACGTGCGGCCGAGA 400  
DB 82 ...H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SC.BB.MRTWMC.D.M.SN. 23  
QY 401 TTC 403  
DB 22 .TS 20

RESULT 6  
US-10-142-885-34/c  
; Sequence 34, Application US/10142885  
; Publication No. US20030157604A1  
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc

```
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C248
CURRENT APPLICATION NUMBER: US/10/142,885
CURRENT FILING DATE: 2002-05-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-142-885-34
```

```
Query Match 6.6%; Score 35; DB 15; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCGCATTTGATGATATATTTGCTGATATCATTTCTCGAATCGGCATCAGA 160
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS....S..N.S..Y.SDK. 263

QY 161 GCAGGCTCATTAACGATAAAGAAATGTTGTTGAAGGCAAGCATGACCACTTGCAC 220
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 KYA..RB.MNK..WSTA.RG..AKSCHRA..SSA..R...N.C...RTHNRA.YA..AH 203

QY 221 CATCAATCAAGAACAAACAGAGATGCAATCATATCATGAGCCAAATGTTGTAAGG 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 YN.KYN...NSSHSBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143

QY 281 CAGATGCTATCTCCATGAGGAAATGTCATCAACATCTGTTAAGCGGCTATATAAG 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRACSBMYCCAN.Y..A 83

QY 341 CCAGGTCATCTTGTGCTCGGCGTCCGCTCTACATATGTTGTGACGTGCGGCCAGA 400
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 ...H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWC.D.M.SN. 23

QY 401 TTC 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 .TS 20
```

```
RESULT 7
US-10-158-790-34/c
Sequence 34, Application US/10158790
Publication No. US20030180879A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
```

```
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C448
CURRENT APPLICATION NUMBER: US/10/158,790
CURRENT FILING DATE: 2002-05-30
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-158-790-34
```

```
Query Match 6.6%; Score 35; DB 15; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCGCATTTGATGATATATTTGCTGATATCATTTCTCGAATCGGCATCAGA 160
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS....S..N.S..Y.SDK. 263

QY 161 GCAGGCTCATTAACGATAAAGAAATGTTGTTGAAGGCAAGCATGACCACTTGCAC 220
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 KYA..RB.MNK..WSTA.RG..AKSCHRA..SSA..R...N.C...RTHNRA.YA..AH 203

QY 221 CATCAATCAAGAACAAACAGAGATGCAATCATATCATGAGCCAAATGTTGTAAGG 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 YN.KYN...NSSHSBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143

QY 281 CAGATGCTATCTCCATGAGGAAATGTCATCAACATCTGTTAAGCGGCTATATAAG 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRACSBMYCCAN.Y..A 83

QY 341 CCAGGTCATCTTGTGCTCGGCGTCCGCTCTACATATGTTGTGACGTGCGGCCAGA 400
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 ...H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWC.D.M.SN. 23

QY 401 TTC 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 .TS 20
```

```
RESULT 8
US-10-137-871-34/c
Sequence 34, Application US/10137871
Publication No. US20030207350A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C153
CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT FILING DATE: 2002-05-03
```

Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 34  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-137-871-34

Query Match 6.6%; Score 35; DB 16; Length 328;  
Best Local Similarity 6.9%; Pred. No. 0.67;  
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCCATTTGATGATATATTTCCGTGATATATTTCCGATCGGATCGATCAGA 160  
DB 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK.263  
QY 161 GCAGGCTCATTAACATTAAGAAATGTTGTTGAAGGACGACATCAGACCTTGAC 220  
DB 262 KYA..RB..MKT..WSTA..RG...AKSCHRA..SSA..R...N.C...RTHMRA..VA..AH 203  
QY 221 CATTCATTCAGAACAAACAGATGCAATCTATCATCTAGCCATCTGTTGAAGG 280  
DB 202 YN.KYN...NSSHBM...SBBB..CN.SMTT..ABNR...DNRD...B.CS..T..CN..D.S 143  
QY 281 CAGATGCTATCTTCATGAGGAAATGTCATGATCTGTAAGCGGCTATATAG 340  
DB 142 C.SH.SC.D.Y...YDSRAK..CCS..NB.D.MH.Y.SBDYCARKACSBMYCCAN.Y..A 83  
QY 341 CAGGTCATCTCTGCTCGGGTCCGCTCTTACATGATTTGTTGACGTCGCCGAC 400  
DB 82 ...H..KDSA..NB.S.YMCBSG..NMTSNB..CW.S.B.B..SC..BB..MRTWMC..D.M..SN. 23  
QY 401 TTC 403  
DB 22 .TS 20

## RESULT 9

US-10-140-923-34/c  
Sequence 34, Application US/10140923  
Publication No. US20030207355A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C188  
CURRENT APPLICATION NUMBER: US/10/140,923  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 34  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-923-34

Query Match 6.6%; Score 35; DB 16; Length 328;

Best Local Similarity 6.9%; Pred. No. 0.67;  
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCCATTTGATGATATATTTCCGTGATATATTTCCGATCGGATCGATCAGA 160  
DB 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK.263  
QY 161 GCAGGCTCATTAACATTAAGAAATGTTGTTGAAGGACGACATCAGACCTTGAC 220  
DB 262 KYA..RB..MKT..WSTA..RG...AKSCHRA..SSA..R...N.C...RTHMRA..VA..AH 203  
QY 221 CATTCATTCAGAACAAACAGATGCAATCTATCATCTAGCCATCTGTTGAAGG 280  
DB 202 YN.KYN...NSSHBM...SBBB..CN.SMTT..ABNR...DNRD...B.CS..T..CN..D.S 143  
QY 281 CAGATGCTATCTTCATGAGGAAATGTCATGATCTGTAAGCGGCTATATAG 340  
DB 142 C.SH.SC.D.Y...YDSRAK..CCS..NB.D.MH.Y.SBDYCARKACSBMYCCAN.Y..A 83  
QY 341 CAGGTCATCTCTGCTCGGGTCCGCTCTTACATGATTTGTTGACGTCGCCGAC 400  
DB 82 ...H..KDSA..NB.S.YMCBSG..NMTSNB..CW.S.B.B..SC..BB..MRTWMC..D.M..SN. 23  
QY 401 TTC 403  
DB 22 .TS 20

## RESULT 10

US-10-141-756-34/c  
Sequence 34, Application US/10141756  
Publication No. US20030207359A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C200  
CURRENT APPLICATION NUMBER: US/10/141,756  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 34  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-141-756-34

Query Match 6.6%; Score 35; DB 16; Length 328;  
Best Local Similarity 6.9%; Pred. No. 0.67;  
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCCATTTGATGATATATTTCCGTGATATATTTCCGATCGGATCGATCAGA 160  
DB 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK.263  
QY 161 GCAGGCTCATTAACATTAAGAAATGTTGTTGAAGGACGACATCAGACCTTGAC 220  
DB 142 C.SH.SC.D.Y...YDSRAK..CCS..NB.D.MH.Y.SBDYCARKACSBMYCCAN.Y..A 83

Db 262 KYA.RB.MNK..MSTA.RG...AKSCHRA..SSA..R....N.C...RTHNMA.YA.AH 203  
QY 221 CATCCAAATCAGCAAAACAGAGATGCACTATTCATACACGAGCCCATGTTGTAAGG 280  
Db 202 YN.KYN...NSSHBM...SBBB.CN.SMTT..ABNR..DNRD...B.CS.T.CN..D.S 143  
QY 281 CAGATGCTATCTTCATATGAGGAAATGTCACACATCTGTAAGCGGCTATATAAG 340  
Db 142 C.SH.SC.D.Y....YDSRAK.CCS.NB.D.MH.Y.SBDYCANRACSBMYCCAN.Y.A 83  
QY 341 CCAAGTGCACTCTTGCTCGGGGTCGCCCTACACATTTGTAACGTGGGCCCA 400  
Db 82 ...H..KDSA..NB.S.YMCBSG..NMTSMB.CW.S.B.B.SC.BB.MRTWMC.D.M.SN. 23  
QY 401 TTC 403  
Db 22 .TS 20

## RESULT 11

US-10-141-759-34/c  
Sequence 34, Application US/10141759  
Publication No. US20030207361A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C197  
CURRENT APPLICATION NUMBER: US/10/141,759  
CURRENT FILING DATE: 2002-05-08  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 34  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-141-759-34

Query Match Best Local Similarity 6.6%; Score 35; DB 16; Length 328;  
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCATTTGACTGATATATTTCCGCTGATATCATTTCTCGGAATCGCATAGA 160  
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS....S.N.S..Y.SDK. 263  
QY 161 GCAGGCTCATTAACCAATAAAGAAATGTTTGTGAAGCAAGCATCAGACCATTTGCAC 220  
Db 262 KYA.RB.MNK..MSTA.RG...AKSCHRA..SSA..R....N.C...RTHNMA.YA.AH 203  
QY 221 CATCCAAATCAGCAAAACAGAGATGCACTATTCATACACGAGCCCATGTTGTAAGG 280  
Db 202 YN.KYN...NSSHBM...SBBB.CN.SMTT..ABNR..DNRD...B.CS.T.CN..D.S 143  
QY 281 CAGATGCTATCTTCATATGAGGAAATGTCACACATCTGTAAGCGGCTATATAAG 340  
Db 142 C.SH.SC.D.Y....YDSRAK.CCS.NB.D.MH.Y.SBDYCANRACSBMYCCAN.Y.A 83

QY 341 CCAAGTGCACTCTTGCTCGGGGTCGCCCTACACATTTGTAACGTGGGCCCA 400  
Db 82 ...H..KDSA..NB.S.YMCBSG..NMTSMB.CW.S.B.B.SC.BB.MRTWMC.D.M.SN. 23  
QY 401 TTC 403  
Db 22 .TS 20

## RESULT 12

US-10-140-805-34/c  
Sequence 34, Application US/10140805  
Publication No. US20030207417A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C176  
CURRENT APPLICATION NUMBER: US/10/140,805  
CURRENT FILING DATE: 2002-05-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 34  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-805-34

Query Match Best Local Similarity 6.6%; Score 35; DB 16; Length 328;  
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCATTTGACTGATATATTTCCGCTGATATCATTTCTCGGAATCGCATAGA 160  
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS....S.N.S..Y.SDK. 263  
QY 161 GCAGGCTCATTAACCAATAAAGAAATGTTTGTGAAGCAAGCATCAGACCATTTGCAC 220  
Db 262 KYA.RB.MNK..MSTA.RG...AKSCHRA..SSA..R....N.C...RTHNMA.YA.AH 203  
QY 221 CATCCAAATCAGCAAAACAGAGATGCACTATTCATACACGAGCCCATGTTGTAAGG 280  
Db 202 YN.KYN...NSSHBM...SBBB.CN.SMTT..ABNR..DNRD...B.CS.T.CN..D.S 143  
QY 281 CAGATGCTATCTTCATATGAGGAAATGTCACACATCTGTAAGCGGCTATATAAG 340  
Db 142 C.SH.SC.D.Y....YDSRAK.CCS.NB.D.MH.Y.SBDYCANRACSBMYCCAN.Y.A 83  
QY 341 CCAAGTGCACTCTTGCTCGGGGTCGCCCTACACATTTGTAACGTGGGCCCA 400  
Db 82 ...H..KDSA..NB.S.YMCBSG..NMTSMB.CW.S.B.B.SC.BB.MRTWMC.D.M.SN. 23  
QY 401 TTC 403  
Db 22 .TS 20

```
RESULT 13
US-10-140-864-34/C
; Sequence 34, Application US/10140864
; Publication No. US20030207419A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C184
; CURRENT APPLICATION NUMBER: US/10/140,864
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-864-34

Query Match      6.6%; Score 35; DB 16; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 96; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCAATGTAATGATATATTTGCTGATATATTTCTGGAATCGGCATCAGA 160
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN...B.Y.NHSKS...S..N.S..Y.SDK. 263

QY 161 GCAGGCTCATTAACCAATTAAGGAAATGTTGTTGAAGGCAAGCATAGACCTTGCAC 220
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 KYA..RB..MNR..MSTA..RG...AKSCHRA..SSA..R...N.C...RTHMRA.VA.AH 203

QY 221 CATCCATCATGCAACAAACAGATGCACTATCATATGAGCCATGTTGTAAAGG 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 YN.KIN...NSSHBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143

QY 281 CAGATGCTATCTCCATATGAGGAAATGTCATCAATCTGTTAAGCGGCTATATAG 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 C.S.H..SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKAOSBNVCAN.Y..A 83

QY 341 CCAAGGTCATCTCTGCTCGGGTCCGCGCTCTACATATGTTGTAGCGGCCCAAGA 400
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 ...H..KDSA..NB.S.YMCBSG.NMYSNB.CW.S.B.B.SC.BB..MRTWMC.D.M.SN. 23

QY 401 TTC 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 .TS 20
```

```
RESULT 14
US-10-142-426-206
; Sequence 206, Application US/10142426
; Publication No. US20040048333A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura

APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C224
; CURRENT APPLICATION NUMBER: US/10/142,426
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 206
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-426-206

Query Match      6.4%; Score 34; DB 13; Length 616;
Best Local Similarity 9.6%; Pred. No. 2.1;
Matches 46; Conservative 124; Mismatches 308; Indels 0; Gaps 0;

QY 18 GGGGAATGTGGAGGAGGAGCTCGGGGGGAATAGCGTCCGCTAATCGCATATAGC 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 RESVNRFGTYPALPSKGGKWEILNFOYERAKKAASLIKGLERFHVGILGFSAE 67

QY 78 TTCTGTAATCATGCTTCTGCTTCCCTTAAGCCGCAATGTAATATTTGCTGATATC 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 WFTTAVGAILAGGLCVGIATNSABACQYITHAKNVILLVENDQQLKLSIPQSLBP 127

QY 138 ATTTTCGGAATGGGATCAAGAGCGCTCATTAACCAATTAAGGAAATGTTGTGAA 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 LKAIIQYRLPMKKNMNLVSWDDPMBELGRSIPDQLBEVIESORANCAVALYISGTGIP 187

QY 198 GGAAGATGACAGACCTTCCACCATCCATCAACGAACAAACAGATGAATCAT 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 KGVWLSHDNITWTAGATTKDFKLTDRHETVSYLPSHIAQMDIWPPIKIGALTYFAQ 247

QY 258 ACTGAGCCATGCTTGTAAAGGCAAGATGCTATCTCCATGAGGAAATGTCATGCA 317
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 ADALKTGLVSTLKEVPTVPIGVPIQWIKHEWVKNSAKSMGLKKAFVMAINIGPKVN 307

QY 318 CATCTGTAAAGCGCTATATTAAGCCAGTGCATCTCTGCTCGGGGCTCGCTCAAC 377
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 SKTMLGKYNTPVSYRNAKTLVFSKVTSLDLDBCHSFISGTAALNDETAFFPLSLDIPIG 367

QY 378 ATTTGTCAGCGCGCGCCCAAGTGAATCTGTATTAAGGCTTTTCTCTATATCT 437
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 ELVGLSESSGPHITISNONNRLILSCGKILTGCKNMLPQONKXDIIGEICLMGRHIFWYLE 427

QY 438 CAGATGGCAGTAGAGAGATTTTGTCTGCTGTTGCTGCTGCTCACTAGCGTGGGCT 495
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 428 SRETTEALIDDEGMHSGDLGQLDGLFLVTHIHEILITTAGENVPIPVETLVAK 485

RESULT 15
US-10-123-155-206
; Sequence 206, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 01:20:42 ; Search time 2498 Seconds

(without alignments)  
6371.714 Million cell updates/sec

Title: US-10-623-891-2

Perfect score: 533

Sequence: 1 tctgaggagagagagtcgagggg.....cgtgagttcgtgtacacaa 533

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

EST:\*

1: em\_ests:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39.4	7.4	1201	9	AL549619
2	38.2	7.2	621	28	BH767965
3	37.8	7.1	654	12	BH767967
4	37.4	7.0	1265	10	BF128543

Result No.	Score	Query Match	Length	ID	Description
5	37	6.9	745	29	BX184525
6	36.6	6.9	1201	13	BX381961
7	36.4	6.8	636	28	AZ572287
8	36.4	6.8	999	29	CNS000H4
9	35.8	6.7	1201	9	AL525502
10	35.4	6.6	456	12	BI350586
11	35.2	6.6	339	12	BI308473
12	35.2	6.6	595	28	BH567971
13	35.2	6.6	798	28	BZ069169
14	35.2	6.6	852	29	CG928645
15	35.2	6.6	962	29	CNS000L9Z
16	35.2	6.6	1101	29	CNS000D88
17	35	6.6	584	28	AQ318844
18	35	6.6	787	28	BZ992571
19	35	6.6	1040	13	BX155200
20	34.6	6.5	456	28	AQ338821
21	34.6	6.5	458	28	AQ641009
22	34.6	6.5	707	28	BZ035991
23	34.6	6.5	1101	29	CNS0160P
24	34.6	6.5	1201	9	AL514124
25	34.4	6.5	539	9	AA504855
26	34.2	6.4	384	28	AQ410136
27	34.2	6.4	500	28	AQ359853
28	34.2	6.4	543	14	CA871192
29	34.2	6.4	616	28	BZ953077
30	34.2	6.4	740	28	AO888634
31	34.2	6.4	838	28	CG674752
32	34	6.4	479	28	AZ164493
33	34	6.4	559	29	CE737197
34	34	6.4	850	29	CG248501
35	34	6.4	898	29	CG248509
36	33.8	6.3	370	9	AV654960
37	33.8	6.3	429	29	CE523584
38	33.8	6.3	494	12	BG275671
39	33.8	6.3	549	13	BQ701682
40	33.8	6.3	623	28	BH765785
41	33.8	6.3	693	28	AQ372284
42	33.8	6.3	892	29	CNS04GZL
43	33.8	6.3	1200	9	AL564823
44	33.8	6.3	1201	9	AL557303
45	33.8	6.3	1842	29	CG756078

## ALIGNMENTS

RESULT 1  
LOCUS AL549619  
DEFINITION AL549619 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
clone CSOD1055113 5-PRIME, mRNA sequence.  
ACCESSION AL549619  
VERSION AL549619.2 GI:31271437  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
JOURNAL 1 (bases 1 to 1201)  
COMMENT On Feb 15, 2001 this sequence version replaced gi:12885780.

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by life technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 8081.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSOD1055113&cluster=8081.r. Contact :  
Peng Liang Email: fliang@lifetech.com URL :

http://fulllength.invitrogen.com/InvitrogenCorporation1600  
Paradise Avenue Genoscope sequence ID : CSDD1055AE07QPL  
Location/Qualifiers

## FEATURES

## source

1..1201  
/organism="Homo sapiens"  
/mol\_type="RNA"  
/db\_xref="taxon:9606"  
/clone="CSDD1055Y113"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_id="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 7.4%; Score 39.4; DB 9; Length 1201;  
Best Local Similarity 41.3%; Pred. No. 0.83;  
Matches 74; Conservative 24; Mismatches 81; Indels 0; Gaps 0;

QY 146 GAATCGCATCAAGAGCAGGCTCTAAGACATTAAGAAATGTTGTGAAGCAGCA 205  
DB 1022 GAACTGGTMCCTAAAGAGCAGGCTGCTGTTGATTAAGCTTGAATAAATA 1081  
QY 206 TCAGACCACTTCACCATCCATCAGACAGACAGATCGAATCATATCTGAGCC 265  
DB 1082 AGAATCCATCTTGTCATSYAMATMCTGAAGCGAGAGATGGAGCTOMTATATMTT 1141  
QY 266 AATGTTGTAAAGGAGATGCTATCTCCATGAGGAGAAATGATGCAATCTCTG 324  
DB 1142 HGGGGGGAAGGGTMBAAKSCAGGGCCAAAGGMAAAACCTTKKASCAGCCTG 1200

RESULT 2  
BH767965/c 621 bp DNA linear GSS 20-MAR-2002  
LOCUS BH767965  
DEFINITION BMBAC372H0477 PSU Brugia malayi Genomic Bac Library 3 Brugia malayi genomic, genomic survey sequence.

ACCESSION BH767965  
VERSION BH767965.1  
KEYWORDS GI:19565729  
SOURCE GSS.  
ORGANISM Brugia malayi

Brugia malayi  
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
Onchocercidae; Brugia.  
1 (bases 1 to 621)  
Whitton,C., Daud,J., Ware,J., Quail,M., Hall,N., Barrell,B.,  
Foster,J., Guillano,D., Slatko,B. and Blaxter,M.  
Genome survey sequences from the human parasitic nematode Brugia malayi

REFERENCE 1 (bases 1 to 621)  
AUTHORS Whitton,C., Daud,J., Ware,J., Quail,M., Hall,N., Barrell,B.,  
Foster,J., Guillano,D., Slatko,B. and Blaxter,M.  
TITLE Genome survey sequences from the human parasitic nematode Brugia malayi  
JOURNAL Unpublished (2000)  
COMMENT Contact: Blaxter M.  
Institute of Cell, Animal and Population Biology  
University of Edinburgh  
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JF, UK  
Tel: +44 131 650 6760  
Fax: +44 131 670 5450  
Email: mark.blaxter@ed.ac.uk  
Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, IACPB, University of Edinburgh, Edinburgh, UK.  
Seq primer: 17 (TAATACGACTCATATAGGG)  
Class: BAC ends.

## JOURNAL COMMENT

## FEATURES source

1..621  
Location/Qualifiers  
/organism="Brugia malayi"  
/mol\_type="genomic DNA"  
/strain="TRS"  
/db\_xref="taxon:6279"  
/sex="Mixed (male and female)"

/tissue\_type="whole parasite"  
/dev\_stage="microfilaria (L1)"  
/clone\_id="Brugia malayi Genomic Bac Library 3"  
/note="Vector: pBAC3.6; Site 1: BamH I; Brugia malayi genomic DNA was partially cleaved with Sau3A I and size fractionated. 7,392 clones were generated with mean insert size ~48 kbp. The library was constructed by Claire Whitton, Blaxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."

## ORIGIN

Query Match 7.2%; Score 38.2; DB 28; Length 621;  
Best Local Similarity 52.1%; Pred. No. 1.5;  
Matches 85; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 117 TCGATATATTTGGCGATATCATTTCTCGGATCGGACATCAAGACAGGCTCATTAACCA 176  
DB 171 TAGATATATTTAGGGGATTAATTTGGTCAAAATCTAATTAATGTTAAGATTGTAAATGA 112  
QY 177 TAAAGGAATGTTGTTGTAAGGCAAGCATCGACCATCTTGACCATCCATCAAGACA 236  
DB 111 AATATTAATTTTCTTTAAGAAACATTTAACAAGGAACATTAATATGATG 52  
QY 237 AACACGAGATCGAATCATATCTGAGCCAAATGTTTAAAG 279  
DB 51 ATCACTTGAATGATGTTTACCGCCGTATGTAATGATGATG 9

RESULT 3  
BI870967 654 bp mRNA linear EST 11-OCT-2001  
LOCUS BI870967  
DEFINITION 603395724F1 NIH\_MGC\_90 Homo sapiens CDNA clone IMAGE:5405813 5', mRNA sequence.

ACCESSION BI870967  
VERSION BI870967.1  
KEYWORDS GI:16044640  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 654)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgrabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHAM2034 row: P column: 06  
High quality sequence stop: 510.

## FEATURES source

1..654  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5405813"  
/tissue\_type="adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH MGC 90"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 7.1%; Score 37.8; DB 12; Length 654;



Best Local Similarity 51.5%; Pred. No. 2.1;  
Matches 87; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 85 ATGATGCTGCTGCTCCCTAGCCGCTTGAATGATATATTTGGCTGATTCATTTCTC 144  
DB 461 ATTACTCTCTGTATCTTTAACTGATTTGGGTTTAACTTAAATTTTATCTTTATTT 520  
QY 145 GGATCGGCATCAAGACAGGCTCATTAACCATTAAGAAATGTTTGAAGCAAGC 204  
DB 521 TTTTGGCACTCAAG 580  
QY 205 ATCAGACCACTTGACCATTCATTCAGCAACAAACAGAGATCGAAGT 253  
DB 581 AAGCAACATTAACCAAG 629

RESULT 4  
BF128543/c 1265 bp mRNA linear EST 24-OCT-2000  
LOCUS 601810690R1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4053479 3',  
DEFINITION mRNA sequence.  
ACCESSION BF128543  
VERSION BF128543.1 GI:10967583  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 1265)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strauberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LML at:  
<http://image.llnl.gov>  
Plate: LILCM892 row: d column: 24  
High quality sequence start: 25  
High quality sequence stop: 124.  
Location/Qualifiers  
1..1265  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4053479"  
/issue\_type="leiomysarcoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_46"  
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the Laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

ORIGIN  
Query Match 7.0%; Score 37.4; DB 10; Length 1265;  
Best Local Similarity 58.6%; Pred. No. 3.7;  
Matches 65; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 343 AGGTGATCTCTGCTGGGGTCCCTCCATCAATGTTTGAAGCGGCCCAAT 402  
DB 836 AAGGGGGTTTGACTCTTGCTGGCGGTAGATATTATTAAGTCCGCCCACTCTGTA 777  
QY 403 GCAATCTGTAATAAAGCTTTTCTTCTATCTCTCAGATTGACATGAGA 453

DB 776 TAACTCGTATATTTGGCTGATCTCCGCCACAGAGATAGATAGAGA 726

RESULT 5  
BX184525 745 bp DNA linear GSS 28-JAN-2003  
LOCUS BX184525  
DEFINITION Danio rerio genomic clone DKEX-186F13, genomic survey sequence.  
ACCESSION BX184525  
VERSION BX184525.1 GI:28016395  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE 1 (bases 1 to 745)  
AUTHORS Humphrey, S.J., Huckle, E. and Durham, J.L.  
TITLE Direct Submission  
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
[humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk) Unpublished  
This sequence was generated from the T7 end of BAC 186F13. 186F13  
is part of the Daniokey BAC Library created by R. Plasterk and N.V.  
Keygene. Further details:  
[http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).  
Location/Qualifiers  
1..745  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-186F13"  
/issue\_type="Testis"  
/note="vector pindigobAC-536"

ORIGIN  
Query Match 6.9%; Score 37; DB 29; Length 745;  
Best Local Similarity 53.0%; Pred. No. 4;  
Matches 79; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 49 AGCGTGGCTGCTGAAGTGCATATTAAGCTTGTATATCATGCTTGCTGCTTACGCCG 108  
DB 164 AGGGCTGATCTTTTGTATATATAGAAATATTTGCTGCGCAGATCCCGAGCAGG 223  
QY 109 CATGTACTGATATATTTGGCTGATATCTTTCTCGAATCGCATCAAGAGAGCTC 168  
DB 224 GTTTATTTATGATTTATTTAGTATATTTGTTTGAATTTCTGTCATTGGAAGAAG 283  
QY 169 ATTAACCATTAAGAAATGTTTGA 197  
DB 284 TTCTTCAG 312

RESULT 6  
BX381961 1201 bp mRNA linear EST 08-MAY-2003  
LOCUS BX381961  
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CSOD1072IF05 3-PRIME, mRNA sequence.  
ACCESSION BX381961  
VERSION BX381961.1 GI:30453007  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genome  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope Sequence ID : CS0D1072CC03NPI.

## FEATURES

source

1. 1201  
Location/Qualifiers

## ORIGIN

Query Match

Best Local Similarity 2.8%; Score 36.6; DB 13; Length 1201;

Matches 13; Conservative 143; Mismatches 302; Indels 0; Gaps 0;

```

QY 12 GCTCCGGGGAATGTGGAGGAGCTCCGGGGGAATAGCGTGGCTGCTTAATCCAT 71
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 905 GGGGKKKKMMYKKKKMMKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 846
QY 72 ATTAGCTTGTATATCATGCTTCTTGTAGCCGCAATGATGATATATTTGGCT 131
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 845 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 786
QY 132 GATATCATTTCTCGGAATCGGATCAAGAGCGGCTCTAAACCTTAAAGAAATGTT 191
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 MNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 726
QY 192 GTTGAAGCAAGACATGACATCTTGCACATCCATCAAGACAAACAGAGATCGAAC 251
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 725 ANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 666
QY 252 TATCATCTGAGACCAATGTTGTAAGGAGAGATGATCTCTCAATGAGGAAATGTC 311
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 665 MNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 606
QY 312 ATGCAACATCTCTTAAGCGGCTATATAGCAGGTGATCTTGTCTGGGTCGCCGTC 371
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 605 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 546
QY 372 CTACACATTTGTTGACGCGGCCAGATTGATCTGTAATTAAGCTTTTCTCTTA 431
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 545 MNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 486
QY 432 TATCCTCAGATTGGCAGTGAAGAGATTTTGTTCGTG 469
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 MNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 448

```

RESULT 7  
AZ572287/c 636 bp DNA linear GSS 15-MAY-2001  
LOCUS 304Pv003 Pv MBN #30 Plasmodium vivax genomic 3', genomic survey  
DEFINITION  
SEQUENCE  
ACCESSION AZ572287.1 GI:13985224  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Plasmodium vivax (malaria parasite P. vivax)  
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
REFERENCE  
1 (bases 1 to 636)  
Carillon, J.M.-R. and Dame, J.B.  
The Plasmodium vivax and P. berghei gene sequence tag projects  
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)  
JOURNAL  
CONTACT: Dame JB  
Dept. of Pathobiology, College of Veterinary Medicine  
University of Florida

2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA  
Tel: 352 392 4700  
Fax: 352 392 9704  
Email: damej@mail.ufl.edu  
Seq primer: M13(-20) forward  
Class: Shotgun.

## FEATURES

source

Location/Qualifiers

1. 636

/organism="Plasmodium vivax"

/mol\_type="genomic DNA"

/strain="Salvador I (Collins, W. 1972. J. Parasitol. 69,

497-598)"

/db\_xref="taxon:5855"

/dev\_stage="asexual blood forms"

/lab\_host="Salimiri boliviensis"

/clone\_lib="Pv MBN #30"

/note="Vector: pBluescript SK(+) vector DNA, phagemid  
excised from lambda ZAP, Site 1: EcoR V, Site 2: EcoR V;  
Host leukocytes were extracted from P. vivax infected  
blood using the following methods: first, infected blood  
was activated by the addition of 0.5 ml of ADP (40mg/ml)  
per 10 ml blood. Then blood was passed over a column of  
acid washed 0.1 mm glass beads, then through a plasmid pur  
filter, followed by passage through a column of pre-wet  
Whatman CRI powder (1:2 ratio volume of blood to CRI1),  
and finally centrifuged through a 50% Percoll density  
cushion. Purified DNA was digested with mung bean nuclease  
in the presence of 44% formamide at 500C as described  
(Vernick, K.D., Imbercki, R.B., and McCutchan, T.F. 1988.  
Nucleic Acids Research 16:6883-6896). Digested DNA was  
blunt-ended using T4 DNA Polymerase and size fractionated  
over a Sepharose CL-2B column. Fractions in the size range  
500bp-4kb were ligated into the Eco RV site of pBluescript  
SK(+), and E. coli XL-10 Gold transformed with the  
ligation mixture."

## ORIGIN

Query Match

Best Local Similarity 6.8%; Score 36.4; DB 28; Length 636;

Matches 88; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

```

QY 31 GGAAGCTCGGGGGAATAGCGCTGCTGCTAATGCTATTAAGCTTGTATCATG 90
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 607 GGGTCCCTCCGGTGATGCTCCCGGGGCTCCCGGGGGTCTCCCTTGAGTAACTTT 548
QY 91 CTGCTGCTTAAGCGGCATTTGATGATATATTTGCTGATATATTTCTCGAATC 150
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 547 TTTTTCCTCCCTATGCTGCTTGGAATAAATTAACCGCTGCGTCACTCACTGAG 488
QY 151 GGCATCAAGACGAGCTCATTAACCATTAAGAAATGTTTGTGAAGGACAGC 204
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 487 GGAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434

```

RESULT 8  
CNS00HK4/c 999 bp DNA linear GSS 03-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence 77 end of BAC:  
DEFINITION BACR35P15 of RPCT-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL073686  
VERSION AL073686.1 GI:4953365  
KEYWORDS  
SOURCE  
ORGANISM  
Drosophila melanogaster (fruit fly)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephyritroidea; Drosophilidae; Drosophila.  
REFERENCE  
1 (bases 1 to 999)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr



Query March	6.6%;	Score 35.4;	DB 12;	Length 456;
Best Local Similarity	52.3%;	Pred. No. 11;		
Matches 78;	Conservative	0;	Mismatches 71;	Indels 0;
				Gaps 0

QY	49	AGGCGTGGCTCGTAACGCAATATTACCTTCTGTAATCATGCTTGCTGCTTACCCG	108
Db	308	AGGCGTGAATCTTTAGTATTAATATAGAACTCTTTGTTGCGCAATCTCCAGCAG	367
QY	109	CATCTACTGATATATTTCGCTGATATCATTTCTCGAATCGGATCAAGACAGCTC	168
Db	368	GTTTATTATTAGTTTATTATAGCAATATAGTTTTTGGAATCTGTCATGTGAAGANG	427
QY	169	ATPAAACATPAAAGGAATGTTGTGAA	197
Db	428	TTCTTCAGAAAGAACCCGTTTTTTGAA	456

RESULT 11	339 bp	mRNA	linear	EST 20-JUN-2001
B1308473				
LOCUS	B1308473			
DEFINITION	EST1259883	GPOD	Medicago truncatula	cDNA clone pGPOD-7A11 5' end,
ACCESSION	B1308473			
VERSION	B1308473			
KEYWORDS	B1308473.1	GI:14982800		
SOURCE	EST			
ORGANISM	Medicago truncatula (barrel medic)			
	Medicago truncatula			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 339)	Grunsk, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utechtack, T., Cho, J., and Fraser, C.M.	ESRs from developing reproductive tissues of Medicago truncatula	Unpublished (2001)	Contact: Michael A. Grunsk

## FEATURES

```

/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
/clone="pGPD-7A11"
/tissue_type="Immature pod walls"
/dev_stage="Immature pods, ranging in age from 15 to 30 days after pollination"
/clone_lib="GPD0"
/note="Vector: pBluscript SK-; Site 1: EcoRI; Site 2: XhoI; Immature pods, ranging in age from 15 to 30 days

```

after pollination, were collected from greenhouse-grown plants. At harvest, seeds were removed from pods and isolated pod walls were collected and immediately frozen in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA<sup>+</sup> enriched RNA. The cDNA was directionally ligated into the unzip xR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-aassist helper phage and propagated in XLDR cells."

Query Match	6.6%	Score 35.2;	DB 12;	Length 339;
Best Local Similarity	57.1%	Pred. No. 11;		
Matches 105; Conservative	0;	Mismatches 73;	Indels 6;	Gaps 2;

QY AGTCCGGGGGGAATAGCGCTGAGCTGCTAACTGCCATATTAGCTTCTGTATCAGCTT 93  
 Db ACCGCGGGGGGAGATTCAACGCGCTCGCTCTCCGCTCGGAGATTCGTATCAT -CAT 106  
 QY GCTTGCGCTTAGCGCGCATTTGTACTGTATATATTT-----CGCTGATATCATTTTCTCGAA 148  
 Db GACTCCCATTCAGCTATTGACGTGATGATGTTGCTGAGCGCTGAAATTCATCTCTGAT 166  
 QY TCGGCATCAAGAGCAGGCTCATTAACCATTAAGAAATGTTGTGTAAGCGAAGCATCA 208  
 Db TTCTGATGAAGAGCATGATCATGAACGTGAATTTGAAATGATCATCATTCATTCATCA 226  
 QY GACC 212  
 Db GACC 230

Accession	Definition	LOCUS	Result 12
BH567971			
BH567971	BOHG95TF BOHG Brasilia oleracea genomic clone BOHG95, genomic survey sequence.	595 bp	DNA linear GSS 14-DEC-2001

**REFERENCE**  
Town, C.D., Van Aken, S., Utecherak, T., Koo, H. and Fraser, C.M.  
**AUTHORS** Whole genome shotgun sequencing of *Brassica oleracea*  
**TITLE** Unpublished (2001)  
**JOURNAL** Other GSSs: BGGHG05NR  
**COMMENT**

Email: [cdtown@tigr.org](mailto:cdtown@tigr.org)  
DNA is from a doubled haploid provided by Tom Osborn  
Seq primer: TF  
Class: sheared ends.

FEATURES	Location/Qualifiers
source	1. .595

```

/note="Vector: pHS01; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHS01 using BstXI linkers"

```

Query Match

6.6%; Score 35.2; DB 28; Length 595;

Best Local Similarity 58.7%; Pred. No. 14;  
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 114 TACTGTATATTTTCGCTGATATCATTTTCGGATGCGATCAAGACGAGCTCATAA 173  
Db 37 TACAAAGTTACGACGAGGATTAATTTTCATATCTTATCAAGAGTAGACATTAAC 96

QY 174 CCATTAAGGAAATGTTGTTGAAGCAGATCAGACCACTTG 217  
Db 97 ACAACATCAATATTTTCGAAAGAAAGATATACAGAGCTTTG 140

RESULT 13  
BZ069169/c  
LOCUS  
DEFINITION 798 bp DNA linear GSS 10-OCT-2002  
1kh07g11.b1 B.oleracea002 Brassica oleracea genomic, genomic survey  
ACCESSION BZ069169  
VERSION BZ069169  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 798)  
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,  
Nash, W., Rabinowicz, P.D. and Wilson, R.K.  
Whole genome shotgun reads from Brassica oleracea  
Unpublished (2002)  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: rk.wilson@wustl.edu  
Plate: 1kh07 row: 9 column: 11  
Seq primer: -21UPOT forward  
Class: shotgun  
High quality sequence start: 67  
High quality sequence stop: 508.  
Location/Qualifiers  
1. 798  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3712"  
/clone\_lib="B.oleracea002"  
/note="Vector: pOTW13; Whole genome shotgun library from  
flowering buds. DNA was purified from a crude nuclear  
prep using Brassica oleracea T0100DH3 buds, provided by  
Thomas Osborn at the University of Wisconsin. Genomic  
DNA was provided by Pablo Rabinowicz (CSHL) and the  
shotgun library prepared at Washington University Genome  
Sequencing Center."

ORIGIN

Query Match 6.6%; Score 35.2; DB 28; Length 798;  
Best Local Similarity 60.4%; Pred. No. 15;  
Matches 59; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 84 AATCATGCTTGGCTTCCCTTAAAGCCGCAATGATATATTTTCGCTGATCATTTCT 143  
Db 472 AATCATGCTTGGCTTCCCTTAAAGCCGCAATGATATATTTTCGCTGATCATTTCT 413

QY 144 CGGAATGCGATCAAGACGAGCTCATTAACCATTA 179  
Db 412 CTGAATTTAAAAAATAATTCATTCATTA 377

RESULT 14  
CG928645/c  
LOCUS  
DEFINITION 852 bp DNA linear GSS 12-DEC-2003  
MBHFJ36TR mch2 Medicago truncatula genomic clone 55824, genomic  
survey sequence.  
ACCESSION CG928645

VERSION CG928645.1 GI:39790532  
KEYWORDS GSS.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.  
1 (bases 1 to 852)  
Town, C.D., Shetty, J., Koo, H. and Feldjany, T.F.  
Sequencing of BAC ends from Medicago truncatula  
Unpublished (2003)  
Other GSSs: MBHFJ36TR  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
Seq primer: TGTAAACGACGGCCAGT  
Class: BAC ends  
Location/Qualifiers  
1. 852  
/organism="Medicago truncatula"  
/mol\_type="genomic DNA"  
/cultivar="genotype A17"  
/db\_xref="taxon:3880"  
/clone\_lib="55824"  
/note="Vector: pBelOAC11, site 1: HindIII, site 2:  
HindIII, Cook, D.R. and Kim, D.J., unpublished"

ORIGIN

Query Match 6.6%; Score 35.2; DB 29; Length 852;  
Best Local Similarity 47.7%; Pred. No. 16;  
Matches 103; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 111 TTGACTGATATATTTTCGCTGATATCATTTTCGGATGCGATCAAGACGAGCTCAT 170  
Db 611 TTTTCTTATATATGCTCTTAATCAACTTTTGTGTTCTTCTATAGTAATTTGGTAC 552

QY 171 AAACATTAAGAAATGTTTGTGAAGGCAACATCAGACCACTTGCACCATTCATCA 230  
Db 551 GTGAGGAAAGAAAGATGATGCTTGAAGTGAACCTGTCACTGACGCAATTAACCA 492

QY 231 CGAACAAACGACGATGCAATCTATCTACTGACCAATGTTTAAAGGCAATGCTAT 250  
Db 491 CGACAAAGATTGAACACTGCTATGTATGACCAATGAAGTAAGTCTATATCTC 432

QY 291 CTTCCATGATGGAATATGTCATGCAACATCCCTGTA 326  
Db 431 AATCCCTATAGCCAGTGTGCTCCCAATATCTGTA 396

RESULT 15  
CNS00192/c  
LOCUS  
DEFINITION 962 bp DNA linear GSS 02-JUN-1999  
Drosophila melanogaster genome survey sequence JET3 end of BAC:  
BACR24H08 of RPL1-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL068054  
VERSION AL068054.1 GI:4958184  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 962)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

